U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

را بالمهام (۱۹۹۵) افتارهای بهمانی کاران

| Requestor's Name: | | | Serial Number: _ | | |
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| Date: | | Phone: | | Art Unit: | 1 |
| | led statement of search e a special meaning. G y of the sequence. You | ive evennies of feleve | nt citations, authors, | . Keywolus, etc., ii r | noe searched. Define any known. For sequences, 1(s). |
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| Number of Search | nes: | | A.A. Seque | nce | SDC DARC/Questel |
| Number of Datab | ases: | · · · · · <u>-</u> | Structure Bibliograph | nic · | Other CGN |



STIC Database Tracking Number: 97680

To:

Phuong Bui

Location: CM1-9E12

Art Unit: 1638

Tuesday, July 08, 2003

Case Serial Number: 09/938294

Beverly Shears From:

Location: Biotech-Chem Library

CM1-1E05

Phone:

308-4994

beverly.shears@uspto.gov

| Search Notes | ¥ . |
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

ALIGNMENTS

| REFERENCE AUTHORS | ACCESSION VERSION KEYWORDS SOURCE ORGANISM | RESULT 1 AC024609/c LOCUS DEFINITION |
|---|--|--|
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Inchephyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 90341) Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., | AC024609 AC024609.2 GI:7212002 HTG. Arabidopsis thaliana. Arabidopsis thaliana | ACO24609 90341 bp DNA linear PLN 12-SEP-2000 Arabidopsis thaliana chromosome I BAC F14P1 genomic sequence, complete sequence. |

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REFERENCE
AUTHORS
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gene
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                                                                                                                                                                                                                                                                                                                                                                 Genes with similarity to proteins in the databases are named putative, '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSAN (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW.html), and NetPlantGene (S.M. Hebbgaard, et al., CBS, Technical University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Direct Submission
Submitted (12-SEP-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                        (S.M. Hebsgaard, et al., CBS, Technical Universit
Denmark, http://www.cbs.dtu.dk/NetPlantGene.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Mar 9, 2000 this sequence version replaced gi:7121532. Bases 1-59,676 of IGF clone F14P1 overlap with IGF clone F6F9, gb|AC007797.

e-mail for correspondence: arab@sequence.stanford.edu
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Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A.
and Davis, R.W.
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Submitted (11-AUG-2000) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
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Submitted (09-MAR-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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Pederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Buehler, E., Chin, C., Chiou, J., Choi, E., Dunn, P., Gonzalez, A., Howng, B., Kim, C., Koo, T., Lee, J.M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P., Thaveri, A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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Submitted (01-MAR-2000) DNA Sequencing and Technology Center, Submitted (01-MAR-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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region."
                                                          /note="overlap
GenBank record
                                                                                                                                                        clone="F14P1"
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                        .90341
.61960
                                                       with IGF clone F6F9, gb/AC007797, for BAC clone F6F9 for annotation
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A., Ecker,J., Theologis,A.
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RRIRYGSCFRTSLFGBTHVFLSTTESARLVLNNDSGMFTKRYIKSIGELVGDRSLLCA
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74552. .76417
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                                                                                                                                                                          note="Unknown protein"
                                                                                                                                                                                                                                                                              /gene="F14P1.5"
                                                                                                                                                                                                                                                                                                                                                                                   VKYLGENQKVLDILIEEQSQITKKASNKPFLELEDLSEMPYASKMVKESLRMASVVPW
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/gene="F14P1.3"
join(70742. 70816,70957. .71382,72084. .72173,72904. .73284)
/gene="F14P1.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F14P1.4"
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/gene="F14P1.1"
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F14P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAF98407.1"
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/note="Unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="F14P1.1"
|oin(60210. .60
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.75987,76159. .76245,76328. .764
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.76417)
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Query Match
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Matches 702
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46611 GTAACACAGGATTAAAATGCCTAAAACTTATGTCGTGCACCTAGGAAATAGCAAGGAGTT 46552
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                                                                                                                                                                                                                                                                                   CTAAAGTTCTTCCTAAAGTACTCTGGTGGATTCATGAGATGAGAGGTCACTATTTCAAAC 46792
                                                                                                                                                                                                                                                                                                                                                                                                              CTAAAGTCCTTCCGAAGATTTTTGTGGTGGATCCATGAAATGCGTGGGCATTACTTTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTATCTTAAACACTGCTGTTGCTGGCAAGTGGCTTGACCCTGTTCTGAAAGATCATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAGGTGATATCAGCAAAGAGTCAGAAAGCTATAGATACAGCTCTCAAGTCTGATCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCAGGTTTTACCAGCTAGAGGACAGGAGGCAGTTGATATTGCTCTAAAAGCTGATCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGTTTTAAACACTGCTGTTGCTGGGAAATGGCTTGATGCAGTTCTCAAGGACAATGTTC
                                                                                                                                                                                      CTGAATACTGGAAGAACAGAACTCATGATCGCTTAGGGTCTGTTTCCTCTGTAGAGTC 46672
                                                                                                                                                                                                                                  CTGAGTATTGGAATAGCAGGACTAGCGATCGC-----
                                                                                            TTGCGATATATTAGTTTACGTTATTGTCATAAGCTTAACAGTGTTTATTCTTTTATTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                            -CTGAAAATACAGATGCCACAAACTTATGTTGTTCACCTGGGGAATAGTAAAGAACT
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complement(join(81552...81800,81920...82031,82136...8223
82329...82436,82543...82581,82670...82741,82820...83068,8325...8365))
/gene="F14P1.7"
/gene="F14P1.7"
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STVTPPDSYNMSKFEDVGYVNNSTYRENVPAPQAWADDVPDLONGGVPHWONG
HITRASGYDDDLEMGYTHAASGYDDRVHYWEIGAVPQWONDDVPDLONGGVPHWONG
SVSQLQNSDVPQWQNGGVLQLQNGDVPQWQTGGVSQLQNGVHEPQNGIVQKKGSRDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (85358. .87513)
/gene="F14P1.8"
complement (join(85358. .85648,86056.
87001. .87144,87399. .87513))
/gene="F14P1.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Translation="MVNEALPKCPEAPLVLGLOPAALIDNVAPVDMSLLDQIPGDRGG
$IAVQKDELEHMIKELDAHISVAPLKKWAGGSVTMYVRGLSVGGVAFKGIIGAYGDDE
GGQLFVSNMGFSGVS1STLAKKKKGSTACVCLUNDSGNRYMFPCLSSAVKIQABLSK
EDFTGSKMLVLRYAVLNLQVIQAAIRFAKQEGLSVSLDLASFEMVRNSKSELRQLLES
GNIDLCFANEDERAELLRGEGEAGPEAALFLGKGKGSTAKHDKEVVH
ISAIGETVATDAMTGAGDLFAAGFLYGLIKGLSLEECCKVGSCSGSVIRALGGEVTPE
HISAIGETVATDAMTGAGDLFAAGFLYGLIKGLSLEECCKVGSCSGSVIRALGGEVTPE
MQQMMHKQLQLKGLEVPDIHN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similar to defensin; Similar to defensin AMP1 (antimicrobial protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MMAVEGRICERRSKTWTGFCGNTRGCDSQCKRWERASHGACHAQF9GFACFCYFNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGRHRHRHGHRSRKHRQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAF98405.1"
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/codon_start=1
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Pred. No. 2.4e-50;
0; Mismatches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 207; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 90341;
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                                                                                                                   SOURCE
ORGANISM
     REFERENCE
AUTHORS
  Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II, Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 119942)
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
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S 밁 Ś 밁 δ В Ś 뮍 8 밁

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| RESULT 2 AC007797/c LOCUS AC007797 DEFINITION Arabidopsis thaliana chromosome complete sequence. ACCESSION AC007797 VERSION AC007797.7 GI:7839909 KEYMORDS HTG. | 771 CAAAAATTCACTC 4 | 1462 CACAGGAGCACTC 1474 | 45831 TCTTGGAACATCATATGTCTCATCGA | 1402 TCATGGAGCACCACATGGCTGAGAGC | 45891 CTAACGTGAAGATGAGGAATACAATK | 1342 GCCACGCCGAGCAGAGGGTCTCCATO | 45951 TGCACAACACTGGTAAAGATGGCGTC | 1282 TGCATCCTGCTGGGAAGGAGGGCGTC | 46011 TACTTGGGACTGCAGCAGGAGGCACA | 1222 TATTGGGCACGGCTGCTGGAGGGACC | 46071 AAGCCAGAGGAGAATGCTTTGGGAGA | 1162 AGGGCCGTGGAAATGCTTTGGAAGG | 46131 ACAAAACAATGAAGGTAGCACCATAT | 1102 ACAAGACATTGGCAGTGGCCCCTTAC | 46191 AGACAGAGCTACGCAACTTTGTCCAA | 1042 AGACTCAGTTACGTGACTTTGTGGTG | 46251 AGGTACCAACAATGCATGCAGTGGTA | 982 AAGTGCCTAGAATACATGCTGTAGTT | 46311 ATCTATTCCTCCGAGCGTTCCATGAA | 925 ACTTATTTCTTCAAGCATTTTATCAGGCTTTGCAGCTCATCCAACACG | 46371 TTAATTTGCTTTCTGACTGGTGCTTC | 901 | 46431 ATTCTTTCTCTTCCTTAGTTTCTTTA | 901 | 46491 TCTTGGAGTGAGGAATGAAGACATAC | 857 CCTTGGAGTACGGAGTGAGGATCTCCTGTTTGCAATAAAACA- | 46551 GATGGAAGTAGCTGAAGATAGTTTCG | |
|---|---------------------|-------------------------|---|---|--|--|--|--|---|--|--|---|---|---|---|---|--|---|---|--|--|------------------------------|---|-----|--|---|---|--|
| 2 bp DNA linear PLN 12-SEP-2000 some I BAC F6F9 genomic sequence, | | | TCTTGGAACATCATATGTCTCATCGAATAGCTTCTGTGCTCAGAGAAGTGTTGCAACATG 4577 | TCATGGAGCACACATGGCTGAGAGGATCGCGGGGGGTGTTGAAGGATGTCCTGAGGAAAT 1461 | CTAACGTGAAGATGAGGAATACAATGGGGAAGAAAGGGTATGAGAGGGGTAAAAGAGAGATGT 4583 | GCCACGCCGAGCAGAGAGGTCTCCATGGGGGAAAAGGGCTATGGCAGGGTGAAGGAAATGT 1401 | TGCACAACACTGGTAAAGATGGCGTGTTACCTCTCGCCAAAAAACATTGTGAAGCTGGCGA 4589 | TGCATCCTGCTGGGAAGGACGCCTTGGCAAAGAACATCGTCAGACTCGCAA 1341 | ACTTGGGACTGCAGCAGGAGGCACAATGGAGATTGTAGTGAACAGAACAACAACAACTCTAT 4595 | ATTGGGCACGGTTGCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACTGGCCTTC 1281 | AAGCCAGAGGAGAATGCTTTGGGAGAATAACAATTGAAGCCATGGCCTTTAAGCTTCCTG 46012 | AGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAG 1221 | ACAAAACAATGAAGGTAGCACCATATTTAGCAGCTATTGACGTTCTTGTCCAAAACTCCC 4607 | ACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAATTCTC 1161 | AGACAGAGCTACGCAACTTTGTCCAAGAGATGAAACTTCAAAAAATTGTCCACTTTGTCA 4613 | AGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCATTTTGTGA 1101 | GGTACCAACAATGCAGTGGAGTAGGAAGCGATATGAGCGCACAGACGAAATTTTG 4619 | AAGTGCCTAGAATACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCAAATTTG 1041 | ATCTATTCCTCCGAGCGTTCCATGAAAGTCTTAAAGTAATCAAAGAGACTAAGAAACTTG 4625 | GCTTTGCAGCTCATCCAACACGAGAAACTTA 981 | TTAATTTGCTTTCTGACTGGTGCTTCTCTTATGCAGGTGTATCTCGAGGAAAGGGCCAAG 46312 | GTGTATCACGAGGAAAGGGACAAG 924 | ATTCTTTCTCTTCCTTAGTTTCTTTAAGAATCATAATCTGCAAAAGACTCAAAATTTTGG 4637 | 900 | TGGAGTGAGGAATGAAGACATACTATTTTGGCATTATTAATAGTTAGT | TGTTTGCAATAATAAACA 900 | GATGGAAGTAGCTGAAGATAGTTTCGCCAAGAATGTTCTCCGTGAGCAAGTTCGAGAATC 4649 | |

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REFERENCE
AUTHORS
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JOURNAL
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JOURNAL
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Bases 60,267-119,942 of BAC clone F6F9 overlap with bases 1-59,676
of IGF clone F14P1, AC024609 and bases 1-3,490 of BAC clone F6F9
overlap with bases 89,221-92,710 of BAC clone T20H2, AC022472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (12-SEP-2000) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Direct Submission
Submitted (16-MAY-2000) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Buehler, E., Chin, C., Chiou, J., Choi, E., Dunn, P., Gonzalez, A., Howng, B., Kim, C., Koo, T., Lee, J.M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P., Thaveri, A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases I to 119942)

Pederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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Federspiel, N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
and Davis,R.W.
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Submitted (12-JUN-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S., Buehler,E., Chao,Q., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M., Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 119942)
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                                                                                                                                                                                                                                                                                                                         SSSVESF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Arabidopsis thaliana" db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     one="F6F9"
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                                                                                                                                                                           .7091,7183.
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                                                                                                                                                                           .7443,7547.
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14164. .15678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (16924. .17682)
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Best Local
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                                                                                                                                                                                                                                                                                                                  107117
106877 GTAACACAGGATTAAAATGCCTAAAACTTATGTCGTGCACCTAGGAAATAGCAAGGAGTT 106818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAAAGTCCTTCCGAAGATTTTGTGGTGGATCCATGAAATGCGTGGGCATTACTTTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGTTTTAAACACTGCTGTTGCTGGGAAATGGCTTGATGCAGTTCTCAAGGACAATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCAGGTGATATCAGCAAAGAGTCAGAAAGCTATAGATACAGCTCTCAAGTCTGATCTGG 107178
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                                                                                                                                                                                                                                                              CTGAGTATTGGAATAGCAGGACTAGCGATCGC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F6F9.8"
join(24177. .24
25766. .27256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (31753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYQPRNLNNGNINTSDMQNAKRMRFDRD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F6F9.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .24269,24579. .25172,25331. .25510,25592. .25651,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 282.6; DB 8;
Pred. No. 2.5e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .35330)
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| Qy 1462 | Qy 1 | Qy 1342 | Qy 1282 | Qy 1222 | Qy 1162 | Qy 1102 | Qy 1042 | Qy 982 | Qy 925 | Qy 901 | Oy. 901 | Qy 857 | Qy 797 |
|----------------------------|---|--|--|---|--|--|-----------|---|--|-----------|---|--|--|
| Db 106037 | Db 106 | Db 106157 | Db 106217 | Db 106277 | Db 106337 | Db 106397 | Db 106457 | Db 106517 | Db 106577 | Db 106637 | Db 106697 | Db 106757 | Db 106817 |
| 462 CACAGGAGCACTC 1474 | 1402 TCATGGAGCACCACATGGCTGAGAGGATCGCCGGCGGTGTTGAAGGATGTCCTGAGGAAAT 1461 | 1342 GCCACGCCGAGCAGAGGTTCTCCATGGGGGAAAAGGGCTATGGCAGGGTGAAGGAAATGT 1401 | 1282 TGCATCCTGCTGGGAAGGAGGGCGTGGCGCCTCTTGCAAAGAACATCGTCAGACTCGCAA 1341 | 1222 TATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACCTGGCCTTC 1281 | 1162 AGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAG 1221 | 1102 ACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGATGTGCTTGTCAGAATTCTC 1161 | | 982 AAGTGCCTAGAATACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCAAATTTG 1041 | 925 ACTTATTCTTCAAGCATTTTATCAGGCTTTGCAGCTCATCCAACACGAGAAACTTA 981 | 901 | 901 900 901 ATTCTTTCTCTTAGGTTTCTTTAAGAATCATAATCTGCAAAAAGACTCAAAATTTTGG 106638 | CCTTGGAGTACGGAGTGAGGATCTCCTGTTTGCAATAATAAACA | 797 AATGGAAGTTGCTGAAGACAATGTCGCCAAGAAGATGTCCTACGGGAACATATTCGTGAATC 856 |

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Arabidopsis thaliana chromosome I BAC FIB16 genomic sequence,
Complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                   SdC
                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are named
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'. The
gene prediction programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://genes.mit.edu/GENSCAN.), FEXA (Victor Solovyev,
http://genes.mit.edu/GENSCAN.), FEXA (Victor Solovyev,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
On Max 9, 2000 this sequence version replaced gi:7143418.

Bases 1-32,040 of IGF clone FIB16 overlap with bases 97,508-129,547 of IGF clone F10A5, gb|AC006434.

e-mail for correspondence: arab@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Federapiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A. and Davis, R.W.

Direct Submission
Submitted (13-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (09-MAR-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://genomic.sanger.ac.uk/gf/gf.shtml), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 100685)

Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,

Altafi, H., Nguyen, M., Lam, B., Southwick, A., Bei, C., Buehler, E.,

Chin, C., Chiou, J., Choi, E., Dunn, P., Gonzalez, A., Howng, B., Kim, C.,

Koo, T., Lee, J.M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S.,

Mukharsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P.,

Thaveri, A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J.,

Theologis, A. and Davis, R.W.
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Rederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Pederspiel, N.A., Palm, C.J., Southwick, A., Bei, O., Buehler, E., Chin, C., Chiou, J., Choi, E., Dunn, P., Gonzalez, A., Howng, B., Kim, C., Koo, T., Lee, J.M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P., Thaveri A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

Direct Submission

Cubattral (12 cm.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S Buehler,E., Chao,Q., Chin,C., Chiou,J., Choi,E., Gonzalez,A., Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M., Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 100685)
                                                                                                                                                                                                                                              /note="overlap with bases 97,508-129,547 of IGF clone F10A5, gb|AC006434. See GenBank record for BAC clone F10A5 for annotation in this region." complement 32986. .33822)
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/gene="F1B16.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                 note="Unknown protein; unknown protein"
                                                                                                                                                                                                                            'gene="F1B16.1"
                                                                                                                                                                                                                                                                                                                                                                                                .32040
                                                                                                _start=
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                                                                                                          gene
                                              CDS
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SSVSSNGSVLYCLEITKNYHDSDSEIVQDEWEILMKKLNFIFTSVFTTDLQYVDFLDR
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KWDERSSAVTPDEEVFYLVALLRSALTDGEETQKLEYLKOQNRRILEFCEQAKINVKQ
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A new!"
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LHBSAGEGGVFLAKNIVKLATQVELRLRMGKNGVERVKEMFLEHHMSHRIASVLKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(54491. .56307)
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complement(join(54491. .55074,55197.
55872. .56014,56253. .56307))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Hypothetical protein"
/codon_start=1
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47773. .47875,47963. .48066,48156. .4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55872. .56014,56253. .56307))
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LLQSDLRFGVVYSDSVSGSAÆVGCVOEVVKHERLVDRFFLVKKGERFRVTNVVRT
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PTPFSFFVGSTFEGAPREQQALLELEDTAARLKRERETLRVTLNYLTAASAVKDVFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F1B16.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F1B16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F1B16.2"
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join(43756. .44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .52584,52917. .53501)
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.48185))
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                                                                                                                                                                                                                                                                                                                                          54894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATCCAACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAGTTGTGGGAAGTGATG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTATCACGAGGAAAAGGGACAAGACTTATTTCTTCAAGCATTTTATCAGGCTTTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATCAAAGAGAAACTTCAGGTACCAACAATGCATGCAGTAGTAGTAGGAAGCGACA 54955
                                                                                                                                                                                                                                                                                                                                       AGAACTTTGTCCACTTCGTCAACAAAAACTCTAACCGTAGCACCATATATAGCAGCCATAG 54835
                                                                                                                                                                                                                                                                                                                                                                                         ATGACCGTGTCCATTTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGCAAGCAGACAAAGTTCGAGACAGAGCTACGCAACTTTGTCCGAGAAAAGAAACTTG 54895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAATGCTCAGACCAAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTC 1080
TGAATGGAACGACTGGTCTGTTACATAGTGCAGGGAAAGAAGGAGTGATACCTCTCGCCA 54655
                                                                                                                                               CAATGGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGACCACGGAGATCGTCC 1260
                                                                                                                                                                                                                                                                               ATGTGCTTGTTCAGAATTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAG 1200
                                                 TGGACGGCTCGACTGGCCTTCTGCATCCTGCTGGGAAGGAGGGCGTGGCGCCTCTTGCAA 1320
                                                                                                          CCATGGCCTTTAAGCTACCTGTACTTGGTACTGCAGCCGGAGGAACAATGGAGATTGTAG
                                                                                                                                                                                                                          ACGITCITGICCAAAACTCCCAAGCCAGAGGAGAATGCTTTGGGAGAATAACAATCGAAG 5477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Translation="MPFRIRVSCPDFPRNLSLFWRRVADEIEGSPYYSFYVASRGISM DKMSLGSERGTLSEGGTPPOGLICTPASQKSATPENSTRUKPPSGSSCSLASSDLIEV KNIVDSPGIVEBAQSKDIFSTPSLFWYSDLSSATFRLLPFKSTPSBRARRSPGDLFF RQVSDSQILGLKSFINNYSISEGRSSFVLSTCSNDFATGSQYASSEGGWSMNTFSELV AYSQRDRWSFDSEHLGSGRSKSFSFVLSTCSNDFATGSQYASSEGGWSMNTFSELV AYSQRDRWSFDSEHLGSGRKKLGGGSSRFSFSPVUDQV(CGACSKLITERASIAFTE LPIAAVLACGHVYHAECLETWTTDIEKYDPACPICTIGEKFVAKITRKALKAEABAKA KQYKRCKNRVUDSYGESGLOEFVFQKWGKREGKALKLEASCSSKSSNKSFLKWHFASISKWNKPSKDSALKKGFWSRHNNRSSSSIEVKIHTLNIQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSGFVSSYLRSRYLKPTQQLLDEVVSVKKDLKLGNKKMKNDKGQDFHNGSSDN1TEDD
KSQSQELSPSERQELQSKKSKLLTMVDEVDKRYNQYHHQMEALASSEMVTGLGAAKP
YTSVALNRISHERCLEDAIKEQIQVIRGKLGERETSDEGERIPRLRYLDQRLRQQR
ALHQQLGNVRPAMRQQRGLEDENSVSILRAMIFEHFLHFYPKESBKIMLSKQCTSLSKNQ
VANWFINARVRLMKPMIEEMYKEEFGESAELLSNSNQDTKKMQETSQLKHEDSSSSQQ
QNQENNNNNIFYTSDAEQNLVFADPKEDRATTGDYDSLMNYHGFGIDDYNRYVGLGNQ
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GDVRNNEMVFIPPTSDVAVNGNVTVSSNDLSFHGGGLSLSLGNQIQSAVSVGFYNNYKK
QNLSNQLSYNNLNPSTMSDENGKSLSVHQHHSDQILPSSVYNNNKGNNGVGFYNNYKK
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64640. .64698))
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/gene="F1B16.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /proteIn_id="AAG13064.1"
/db-xref="GI:10120439"
/db-xref="GI:10120439"
/translation="MGSSTEGONCSSVSTTGLANSGSESDLRQRDLIDERKRKRKQSNR
ESARRSRMRKQKHLDDLTAQVTHLRKENAQIVAGIAVTTQHYVTIEAENDILRAQVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(69063. .69566)
/gene="F1B16.8"
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/db_xref="GI:10120440"
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/db_xref="GI:10120442"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 253.4; DB 8; Length 100685; Pred. No. 5e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homeodomain proteins"
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AP001366/c
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-MWR-2000) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai Agrobiological Resources, Rice Genome Research Program; Kannondai (E-mail:tsasakisabr.affc.go.jp, UKL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The orientation of the sequence is from SP6 to T7 of the PAC clone. Genes were predicted from the integrated results of the Genes were predicted from the integrated results of the following:GENSCAN1.0, BLASTW2.0, BLASTW2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNA bank and the CNA sequence database at RGP. Protein similarities of the cording regions were searched against NRP with BLASTP2.0. ESTs represent the identified CDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54594
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Oryza sativa (japonica cultivar-group)
PAC clone:P0469E09.
AP001366 BA000010
AP001366.1 GI:7228436
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Okaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki, T., Matsumoto, T. and Yamamoto, K. Oryza sativa nipponbare (GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone: P0469E09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation of this entry at
http://www.dna.affrc.go.jp:82/genomicdata/GenomeFinished.html..
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Only in Database (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone: P0469E09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detailed information on overlap and assemble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . and RGP clone ID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 146081)
                                                                                                                                            translation="mgavkrssfllvvvvfalllltsmaaggrkmlinkhqvqsmets
ddesmhqqqeddemlamvherilrqvktndygtydptptmakehakeipn"
join(10528. .12588,12673. .13083,13175. .13473,13550. .1
13901. .14083,14241. .14306,14743. .15045,15216. .15479)
/note="EST C28952(C62945) corresponds to a region of the
                                                                                                                                                                                                  /protein_id="BAA92397.1"
/db_xref="GI:7228437"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa (japonica
/cultivar="Nipponbare"
                                                                                      'note="5' LTR"
                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                        oin(5902. .5980,6229. .6272,8134.
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                     clone="P0469E09"
                                                                                                                                                                                                                                                                                                                                                                                 chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:39947"
                                                                                                                         .9989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (cultivar:Nipponbare) DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality together with
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TENIER LEGENSE PULCE AS VULKE 
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/db_xref="GI:728440"
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AITANIESSEDDINLDDWLMELFDPFEDPEGSLAAADLSPDGVBSSNVGALAPKVE
QDVSSSPNUNVVDDTEYLLPEDTVNILHPGTDDFNMLQNFLDGYFIQTAKGTVGINKAATSG
DVSSSPNUNVVDDTEYLLPEDTVNILHPGTDDFNMLQNFLDGYFIQTAKGTVGINKAATSG
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                                                                              complement (join (40209. .4)
/note="EST C28952(C62945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ESTB C96615(C10106),C26336(C12127),D21959(C10106)
Correspond to a region of the predicted gene.
Similar to NAM (AL021889)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLSAVGSHGESSDGWSMRTFSEMVASSORERWSVDSELLGSVSSKMTRSNASNNPTTH
SPPOEVCKLCLKLLKERSTWNAQELAVVAVLLCGHVYHADCLDSLTAEADKYDPPCPV
CTHGEKCTYKLFGKLBSKTKNK, PKNV LVDVNLDGSSKHQKEKI PLEEELYSQARASM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein id="BAA92399.1"
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                                                                                                                                                                                                       omplement(39315, .39726)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSDARWNMILVAGFAIGVAVVALHIGQRLGLSQRDQQHT"
complement(38747. .38998)
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complement (join(27953. .286
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VKSTWYVFEVRCMKEDCPFREVHAVKGKNDYWKVSIVTEHKCYVLGGVEKYHRNITSAF
VASEMYSSVVGNIGFEPKSIIRHIENKFKYTISYVKACRAKQKIIEMRYGTFEASYDN
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/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLTIYKIRYDLHKITTQTE"
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Similar to maize transposon MuDR mudrA protein isolog
(AC003981)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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                                                                                                                                    .40396,40917.
                                                                  corresponds to a region of the
                                                                                                                                           .43545))
Query Match
Best Local Similarity
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CDS

CDS

CDS

13.2%;

Score 224.8; DB 8; Pred. No. 8e-38;

Length 146081;

CDS

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IEGARYAHKDENKEAVKHWAVSCHEERVYKSTNYVEEVROMKEDCHWAVHAVKKWN
DYWKVSI VTEHKCYLOGUEKYHRAITSAFWASEWYSSVUGNIGEERKSI HH ENKEK
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ATGANSSRDISRVKCFNCDEFGHYARQCRKFRRQRRGEANLVQAAEBEPTLLMAHVVG
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GFVQIAARPGGGDGSWIASALLMPRLAAALESDERLGRIFKFVTAEYLGLRPASGSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(58018. .58891,58980. .62098))
/noce="similar to Arabidopsis thaliana chromosome F9013 genomic sequence, putative retroelement pol polyprotein. (AC006248)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein id="BAA92404.1"
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/tr
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/note="3' LTR"
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complement(join(48119 . 48257,48429 . 48703,49975 . 50139))
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/note="Similar to Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, C2-HC type zinc finger protein C.e-MYT1. (AC002986)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKNAEVPSGADASPSGQASDVLFIHMVLEQLMLTTTHFRRCTVVSDPVARTVHNSTHE
KRQLELSLSTFGAAYLHKVNHAHA"
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SIYSWLLAGFRIDQEVYTMSVSVVVSRATEGYFWELMPMDSTDAWRRYVEMAFEWSWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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/codon_start=1
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IIVDEMEREDSDNEEVDDDASSDEEGDVMATDWANEDFSGLVISEGDHVPWEYKENEV
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/db_xref="GI:7228443"
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                                                                                                                                                                                                                                                                                                                                                                                                          id="BAA92406.1"
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiylantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots;
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots,
Spermatophyta, Magnoliophyta; Brassicaceae; Arabidopsis.
                                                                                    Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Olach, H.L., Sakurai, T., Sakur
                                                                                                                                                                                                                                                                                                                                                                                                                                        Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nayven, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamanura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AY091763
AY091763.1 GI:20147190
                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis cDNA clones Unpublished
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Arabidopsis thaliana AT3g15940/MVC8_7 mF
                                        Direct Submission
                                                                      Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAAGACATTGGCAGTGGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATTTGGCTGCAACTGATGTGCTTGTTCAGAACTCTCAGGTGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGAAGAATGGGATTCAGGACCGGGTTCACTTTGTAAACAAGACATTAGCAGTGGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGATGTTAAAATACAGGTGTTTCACGTGGAAAAGGGCAGGACTTATTTCTTCAAGCGTT 12361:
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                                                                                                                                                                                                                                                                                                                                               (bases 1 to 2557)
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(26-MAR-2002) Salk Institute Genomic Analysis Laboratory
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Best Local
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AGGCTACAACTAGGTAGCCAAGGACGTGAAATCGTTGAGAAGATGTACATGAAGCAGCAC 2398
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GSGGAVQMFRSRLLYMLLLITLMTYLGFYVQSRWAHDDDNKVEFLAFGGKLREDVLH
VEQNKRRDLVADAESSHAVVDHTWIVHLGYVQSRWAHTDDNKVEFLAFGGKLREDVLH
VEQNKRRDLYADAESSHAVDHTWIVHLGYVONKRMTYLLAKKEDSTSRRSVSPRRFYRA
SRSSRTRIRSTQKVRKVMETKELDEQDQELPNINVTYGKLFGPFGSLEDRILEWSPQK
RSGTTCDRKSDFKALVWSRRFVLLFHELSMTGAPISWMELASELLSCGATVYAVVLSRR
GGLLQELTRRSLKVVEBKGELSFKTANKADLVIAGSAVCASWIDDYMDHIPAGGSQIA
WMVMENRREYFDRAKFVLDRVGLLIFLSEVQSKQMLTWCEEDHVKLRSQPVIVPLSVN
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479 c 625
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QLLLLESVALALEREQTQEQVAKENQSKIIKNLNGIRKEKISLSARHRLRGSSRKMKI
TSPAVDMHPSVLSATGRRKLLLSGNVTQKQDLKLLLGSVGSKSNKVAYVKEMLSFLSN
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/protein_id="AAM10311.1"
/db_xref="GI:20147191"
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Shinn,P., Chen,H., Cheuk,R., Kin,C.J., Meyers,M.C., Banh,J. Bowser,L., Chang,E., Dale,J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lih,J., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                              Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SIGnAL), Plant Biology Laboratory, The Salk Institute fo Biological Studies, 10010 N. Torrey Pines Road, La Jolla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Genomic Sciences Center (GSC) members carried out the
organism="Arabidopsis thaliana"
|db_xref="taxon:3702"
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ecrega e e a como en c ACATTCGGGAGAGTGACTATCGAAGCAATGGCTTATGGTCTTCCGGTGCTTGGAACAGAT TGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGCT GTTGCCTCATTATACTCCGCAGCAGATGTCTACGTAACAAACTCCCAGGGAGTTGGTGAA 2158 GIGGCCCCTTACTIGGCAGCAATTGATGTGCTTGTTCAGAATTCTCAGGGCCGTGGAGAA 1175 AGGGTCTCCATGGGGGAAAAGGGCTATGGCAGGGTGAAGGAAATGTTCATGGAGCACCAC 1415 AAGGAGGGCGTGGCGCCTCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAG 1355 GCTGGAGGAACAAAAGAGATAGTGGAGCACAATGTTACAGGGCTACTTCATCCTGTGGGG AGGGCAGGTAACAAAGTTTTGGCACAGAATCTTTTGTTTCTTCTTAGAAACCCATCTACA 2338 NGNLSNSVLWTPATTRVASLYSAADVYVTNSQGVGETFGRVTI EAMAYGLPVLGTDAG GTKE I VEHNVTGLLHPVGRAGNKVLAQNLLFLLRNPSTRLQLGSQGRE I VEKMYNKQH Score 89.4; DB 8; Pred. No. 9e-09; 0; Mismatches 146 723 146; Length Indels 2557; 0 Gaps 1235 2278 2218

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                           mRNA
                                                                                                    gene
                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                      http://www.tigr.org/softlab/glimmerm.htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mperteageligr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tglishtml). Annotated genes are named to indicate the level of evidence for their annotation, Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://fp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (19-3AN-2001) The Institute for Genomic Research, Submitted (19-3AN-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, cdtown@rigr.org On Jan 19, 2001 this sequence version replaced gi:12280784.
Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-APR-2000) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 75948)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J., Wu.D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F19K6 genomic sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 75948)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 75948)
Lin,X. and Kaul,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC037424 75948 bp DNA linear PLN 19-JJ
Arabidopsis thaliana chromosome 1 BAC F19K6 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAC clone F19K6 is
The orientation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
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1271. .1360,1454. .1534,1628. .>1723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Kaul, S.
                                                                                                                                                      map="m213"
                                                                                                                                                                                                                                          organism="Arabidopsis thaliana"
|cultivar="Columbia"
                                                                                                                             clone="F19K6"
                                                                                                                                                                                  chromosome="I"
                                                                                                                                                                                                                 db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:12323115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Arabidopsis thaliana chromosome 1 the BAC the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2421
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FLISAILSIMJSESGFECIVVTPAAKRQSLLEBIEREFEAATSLKQLQVDDSTEDKEHCKALF
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12222...12311)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains Pfam profile: PF00658 Poly-adenylate binding protein, unique domain."

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I GGLKQI KVDDSRNLEEESAKRKI I LEEMEREFEEAHSGI NAKADKEESAKKQSGSA I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSKIRVKOKVIKEVLETKOLDDEQDPQLPLTNATYGKLLGPFGSLEDKVLEWSPHRRS
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LKCAFESMKFVDILKVIRWEYQKSCNIKTGGCGESNFVHHFISRCPFVFTIVLEWEKS
ETEKEISETTKALDLELDISRLYVGLEPNTNYRLVSMVGCGEEEEHFCLAYENNRWN
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1271. .1360,1454. .1534,1628. .1723)
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codon_start=1
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PEVLGLGQSGGCSCSKQDEDSSIVIPTKYSIEDILSEESAVQGTETSSLTASLTQLVE

| Query Match 5.2%; Score 87.8; DB 8; Length 75948; Best Local Similarity 53.3%; Pred. No. 3e-08; Matches 185; Conservative 0; Mismatches 162; Indels 0; Gaps 0; Matches 185; Conservative 162; Indels 162; Indels 0; Gaps 0; Matches 185; Conservative 162; Indels 162; I | CDS /gene="F19K6.4" /gene="F19K6.4" /gene="F19K6.4" /codon_start=1 /codon_start=1 /codon_start=1 /product="unknown_protein; 23094-21772" /protein_id="AAG51549.1" /protein_id="AAG51549.1" /db_xref="d1:13323129" /db_xref="d2:13323129" /db_xref="d2:13232129" /db_xref="d2:13323129" /db_xref="d2:13323129" /db_xref="d2:13223129" /db_xref="d2:13223129" /db_xref="d2:13223129" /db_xref="d2:13223129" /db_xref="d2:13223129" /db_xref="d2:13223129" /db_xref="d2:13223129" /db_xref="d2:13223129" /db_xref="d2:132231 | gene complement (217/2240/6) /gene="F19K6.4" mRNA complement (join(<2177223135,2396824076)) /gene="F19K6.4" | /gene="F19K6. /codon_start=- /product="hyp /protein_id=" /db_xref="G1: /translation= LFATIPDRTLPDD | /note="predicted by genemark.hmm" | /gene="r1yk6.15" /codon_start=1 /codon_start=1 /product="beta-glucosidase, putative; 17823-15143" /product="beta-glucosidase, putative; 17823-15143" /protein_id="AAG51546.1" /protein_id="AAG51546.1" /db_xref="gi:12323126" /db_xref="gi:12323126" /db_xref="gi:12323126" /db_xref="gi:12323126" /db_xref="gi:12323126" /db_xref="gi:12323126" /fromsharton="www.refwh.ur.GLALU/TLUGAPTKAPGPVCGAGLDEKFSRLNF /translation="www.refwh.ur.GLALU/TLUGAPTKAPGPVCGAGLDEKFSRLNF /translation="www.refwh.ur.GLALU/TLUGAPTKAPGHCUGAGKIG IQKAPGRCSPYIPODLEDEYGAFIERFWSLANFTHEYGHKYKHWITENEPWFSRAGYDN GKKAPGRCSPYIPOGAGKIGKPTAPTYCDYPOGMKCRYCGAGKIG IAHSPAWFEPODLEHVGGSIERFULAPTYCDYPOGMKCRYCHGKPFN GKLDVYSKGLRYLLKYIKDNYGDFDYIIAHAPTYCDYPOGMKCRYCHGKREFK GKLDVYSKGLRYLLKYIKDNYGDFDYIIAHAPTYCDYPOGMKCRYCHGKREFK GKLDVYSKGLRYLLKYIKDNYGDFDYIIAHAPTYCDYPOGMKCRYCHGKREFN GKLDVYSKGLRYLLKYIKDNYGDFDYIIAHAPGYCGAGAGHCHKKYYIQ RHLLSMHDAICKOKNVYTGYFWSLMDNFEWQDGYKARFGLYYIDFQNNLTRHCKVSG KWYSEFLKPOFPTSKLREEL" 2083921105 Gene="F19862" /gene="F19862" | | | NHRKEKESLLGHRVLTSPSIASSTSESSATSETVETLRAKLNELRGLTARELVTRKDF GQILITAASFEELSSAPISYISRLAKYRNVIKEGLEASERVHIAQVRAKMLKEVATEK QTAVDTHFATAKKLAQEGDALFVKIFAIKKLLAKLEAEKESVDGKFKETVKELSHLLA DASEAYESYHGAVRKAKDEQAAEEFAKEATQSAEIIWVKFLSSL" |
|--|--|--|--|--|--|--|--------------------------------------|---|
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CDS
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                                                                         15655. .17201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(12444. 12474,12682. 12793,13387. 13423,13523. 13592,
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                                                     note="Similar to F6D8.5."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="F6D8.5"
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                                                                                                   ь134. .16170,16281. .16350
.17201)
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                                                                                          enzymes family.
this gene."
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                                                                                                                                                   /note="Is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTRETQRK"
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                                                                                                                                                                                                                                                                                  .30691
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/gene="F6D8.11"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join (25221. .25673, 25912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (tränelation="MASGSINVSGLEFGQINTVYPTGIHKATIVMLHDVGNTGFNSLE
PLQNLRLPNIKWICPTAPRRRVTSLGGBITMAWCDIAKVSENNQDDFGTLMYVNBYIT
SLFSNBPQNVIKGVAGLGLGAAQALYYTSCYAFGKVPINPQIVIGINGMLPGWRCADS
LRMAGFFTLFKQCGGSKHRLLHSFFFFFDYYFLNIHH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD55597.1"
/db_xref="GI:5903038"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (25221. .25968)
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23452 . .23556,23698 . .23830,24195 . .24321)
/gene="FGD8.8"
/note="Similar to F6D8.5."
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VPALESLRHPNIKWIVPTAPMRPVTSIGGEVTTAWCDMTKPSENMLDDFENLNYTNSF
ITSLESSEDDHVMKGVGGIGLGAAQALYYTSCYAFGWVPISPQIVIRINGWLPADDVI
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/db_xref="GI:5903037"
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/protein_id="AAD55623.1"
/db_xref="GI:5903064"
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/protein_id="AAD55622.1"
/db_xref="GI:5903063"
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RPVTSWGGIATTAWCDVTGISENMEDDLVSINSITAFVFSLLLDEPQNGIGGIGLGAA
VALYCATIYISGKKIRNLSFIVGINGWLPAMSSLFIRTQKFGHSSQGWISSHVHTKPR
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20228. .20332,20406. .20531,20797. .20924)
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                                                                                                                                                         a member of the PF|00364 Biotin-requiring amily. ESTs gb|F19971 and gb|F19970 come
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translation="MKYLSLRTTLRSVKAIQLSTVPPAETEAIADVKDSDETKSTVVN/translation="MKYLSLRTTLRSVKAIQLSTVPPAETEAIADVKDSDETKSTVVN THLMPKSSEVPALISEITDSSSIAEFELKLGGFRLYVARKLTDESSPPPQQIQPVVAA

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                                                                                                                                                                                                                                           2 (bases 1 to 147292)
2 (bases 1 to 147292)
28 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bown, A., Burkett, G., Castle, A., Colegel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fithugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, J., Levine, R., Lieu, C., Liu, G., Locke, K., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McMenheeters, R., Meldrim, J., McEwan, P., McGurk, A., McKernan, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1410 CACCACATGGCTGAGAGGATCGCGGCGGTGTTGAAGGATGTCCTGAG 1456
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AC023010 GI:7582616
HTG: BUACCO
                                                            Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 18, 2000 this sequence version replaced gi:6921557. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Smit, A.F.A. & Green, r. (1220-17);
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Similarity 53.3%;
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                                                                                                                                                                                                          Submission
                                                                                                                                                                                                                                  and Zody, M.
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SAMPLING.
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787 31886: gap of 100 bp in length 641 32740: gap of 100 bp in length 185 33584: gap of 100 bp in length 185 33584: gap of 100 bp in length 185 33584: gap of 100 bp in length 185 34353: contig of 769 bp in length 184 335198: contig of 763 bp in length 185 3453: gap of 100 bp in length 185 36161: gap of 100 bp in length 185 36161: gap of 100 bp in length 185 3780: contig of 763 bp in length 185 3780: contig of 763 bp in length 185 3780: gap of 100 bp in length 185 3780: gap of 100 bp in length 186 3780: contig of 763 bp in length 186 3780: gap of 100 bp in length 186 3780: contig of 768 bp in length 186 3780: gap of 100 bp in length 188 40487: gap of 100 bp in length 188 40487: gap of 100 bp in length 187 41373: gap of 100 bp in length 187 41373: contig of 772 bp in length 187 41373: gap of 100 bp 189 4145: contig of 772 bp in length 188 4364: contig of 772 bp in length 187 43052: contig of 772 bp in length 187 43052: contig of 772 bp in length 187 43052: contig of 772 bp in length 187 43054: contig of 772 bp in length 188 43052: contig of 772 bp in length 186 43052: contig of 772
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26599: contig of 778 b,
500 26699: gap of 100 bp
00 27460: contig of 761 b,
61 27560: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24028: contig of 765
24128: gap of 100 b
24872: contig of 744
              43864: gap of 742 bp in length
43964: gap of 100 bp
44694: gap of 100 bp
44794: gap of 100 bp
4554: gap of 100 bp
4730: gap of 100 bp
48202: gap of 100 bp
48102: contig of 772 bp in length
48981: contig of 779 bp in length
49867: contig of 786 bp in length
49867: contig of 786 bp in length
49867: gap of 100 bp
50741: contig of 774 bp in length
50841: gap of 100 bp
51708: gap of 100 bp
52475: contig of 776 bp in length
52575: gap of 100 bp
53113: contig of 767 bp in length
52575: gap of 100 bp
5313: contig of 767 bp in length
52575: gap of 100 bp
5313: gap of 100 bp
5313: gap of 100 bp
5313: gap of 100 bp
54164: contig of 751 bp in length
55263: contig of 751 bp in length
5503: contig of 751 bp in length
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30928: contig of 745 bp
31786: contig of 758 bp
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of 761 bp
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f 781 bp
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Best Local S
Matches 157
Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Eimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burch, E., Brown, M., Bryant, N.P., Chary, C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D. A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Fantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14464 GCCCGCGGGGGAAGGGCCCCGCAGCCCCGCCGGGGGAGCGGGAGCCACCCACCGCG 14405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157;
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Rattus no
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AC109537.3 GI:21737934
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57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 104486)
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56 55955: gap of
6 56713: contig of 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60266: gap of 100 bp
61030: contig of 764 bp in
61130: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No. 0.0018;
0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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SEQUENCING IN PROGRESS
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43965

43022: contig of 13122; gap of 143864; contig of 173964; gap of 174794; gap of 174794; gap of 175564; gap of 175649; gap of 176449; gap of 17730; contig of 17730; contig of 1748102; co

43964:

38664 38763: 37801 37900:

contig of
104 39531: contig of 70
32 39631: gap of
72 40387: cc
74 40487

34454

30183:

29299: 28441:

31028:

0,

Gaps

0

65

185

14345 125

245

14225

27560: gap of 10 28341: contig of 70 28441: gap of 70 28441: gap of 29199: 70

24972:

contig of

25721: cc

49968 50742 50842

11. 11708: gap of 52475: rr

54264: 53413: 52575: 51708: 50841: 49967: 49081: 48202: 47330:

Frantz, P.,

48103

46449: 45564: 44794:

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Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hune, J., Jackson, L. B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Lead, B., Lewis, L. C., Lewis, L. Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Oviedo, R., Pace, A., Patton, B., Pecy, J., Perez, L., Peters, L., Pickens, R., Pimus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Thomas, S., Walliams, G., Williamson, A., Waczyk, R., Washington, C., Walliamson, A., Wu, Y., F., Zhou, J., Zorrilla, S., Wolley, K., Walloy, C., Mu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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On Jul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jul 12, 2002 this sequence version replaced gi:18846856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 5183 bases at least Q40
Consensus quality: 55340 bases at least Q30
Consensus quality: 58186 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: GPZJ
Center clone name: CH230-230E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine Center code: BCM
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1121
2127
2227
3388
           1020:
1120:
2126:
2226:
3387:
3487:
0: contig of 1020 bp in length
0: gap of unknown length
6: contig of 1006 bp in length
6: gap of unknown length
7: contig of 1161 bp in length
7: gap of unknown length
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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                                                                                                                                                       Neurospora crassa
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
               Submitted
                                 German Neurospora genome, project. Direct Submission
                                                                                                                Schulte, U., Holland, R.,
                                                                                                                                                                                                                                                                                                       42273 bp DNA linear PLN Neurospora crassa DNA linkage group II BAC clone B12N19. AL665987
                                                                                          Unpublished
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    (18-JAN-2002) MIPS, Institut fuer Bioinformatik,
                                                                                                       Aign, V., Hoheisel, J., Brandt, P., Fartmann, B., Nyakatura, G., Mewes, H.W. and Mannhaupt, G.
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GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail: G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institut of Biochemistry, Heinrich-Heinerweity, D-40225 Duesseldorf, Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage grand V can be viewed at: http://mips.gsf.de/proj/neurospora. E-mail: ulrich-schulte@uni-duesseldorf.de BAC clone 12N19 (6train OR74A) is available at the Fungal Genetic Stock Center, http://www.fgsc.net Sequencing was performed by MWG Biotech AG, Ebersberg, Germany, ocation/Qualifiers groups Institute

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SOURCE

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BG279736'

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RESULT 11
NCB23H20
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DEFINITION
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Best Local
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Neurospora
Neurospora
Eukaryota;
                                                                                  AL669988.1
                                                                                                    Neurospora
AL669988
                                                                                                                                           NCB23H20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCGAATAATGGTGGACCGACGGAGACGGTGGTGGAAGGGGGAGACGGGGTGGTTGAGAG 37639
                                                                                                                                                                                                                                             ATACGCAGATGGCGGAGAGGTTGGAGGAGAT 37790
                                                                                                                                                                                                                                                                                                                                                                 CCGAGCAGAGGGTCTCCATGGGGGAAAAGGGCTATGGCAGGGTGAAGGAAATGTTCATGG 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCTGGGAAGGAGGCGTGGCGCCTCTTGCAAAGAACATCGTCAGACTCGCAAGCCACG 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACGGCTGCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACTGGCCTTCTGCATC 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAACGAACACTTTGGTATCGTGCCGCTTGAAGCCATGTTAAGGGGCGTGCCGGTGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTGG
                                                                                                                                                                                                                                                                       AGCACCACATGGCTGAGAGGATCGCGGCGGT 1438
                                                                                                                                                                                                                                                                                                                            AGGAAGAGTTGAAGAGGATGGGAAAGAAGGGGGTGGAGAGGGTCAAGGGTAGGTTTGCGG 37759
                                                                                                                                                                                                                                                                                                                                                                                                          ACCCGAATGACGTAGGGGAGTGGGCTAAGGTTATGGATAAGGTTTTGAATGGGATGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="weak similarity to proteinase umuD Salmonella typhimurium, PIR:A36713" (codon start=! /product="hypothetical protein" /protein id="CADD1067.1" /db_xref="GI:18376320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAD21068.1"
/db_xref="GI:18376321"
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FMEKVDKYGMKSGIIKIIPFEEMRSALPFLDELVKQVRVREPIKQEIMGQNGTYRQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="related to regulator of deoxyribodipyrimidine
photo-lyase PHR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similarity to regulator of PHR1,
Saccharomyces cerevisiae, PIR:S50672"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (join (23273. 28743. .29225))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MPTVMGLTTDSSSKTTTTLGNQDLKKPNGGSRLDTISKRNHHAA/KEIETLFWRCLCDDPSAAPEYMAEDCILINPLLSSHPSTTPLSKDSEPNILEVFEKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HQPPARRGERRANAEKTKPAPRSRAAPPAANGTTSNKTPTNTNTGRGKAKGRVTRGSA
KAATDETDDPPITPVSPPPEDEDKPLASIEEEDIKDEACEEEESIPRAGRMGFSRQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PWAGFRFHGDPLVVEIDLMAVALVYKVSLYTVDKKGKGTREVVASVSSSWRQTAGADW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKMQSTSARRKYIRREGSAMIDEAAFKDWDYRMDVSDFTPERCEELERIYWKTLTYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="B12N19.070"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="B12N19.070"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="B12N19.060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="B12N19.070"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon start=1
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  crassa
Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                           crassa
                                                                                                                       122151 l
crassa DNA linkage
                                                                                  GI:18376326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.4%;
50.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58.2; DI
Pred. No. 0.07;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .21062)
                                                                                                                       e group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.07;
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                                                                                                                          DNA
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                                                                                                                            BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 42273;
                                                                                                                          linear PLN
contig B23H20
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                                                                                                                                             PLN 18-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1227
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| intron exon | intron | incron | exon | | | | | | | CDS | gene I | misc_f | 901108 | FEATURES | | | COMMENT | | TITLE JOURNAL | REFERENCE | AUTHORS | REFERENCE |
|---|---|--|-------------|--|--|--|--|---|----------------------------------|---|--------|---|---|----------------------------------|--|---|---|--|--|---|--|--|
| 2152121639 /gene="B23H20.010" /number=3 2164021697 /gene="B23H20.010" /number=3 2169822965 /gene="B23H20.010" /number=4 | H . H . H | μ _. | μ. Β. | GGITVPFYGEAALPMLDPTLYKAEWKALGRHFCDKRDFYVGRLREIGESIKLYPDSTFY LWLNLEWLPGPISDGLNFFQACLEEKVIVVPGIFFDLNPSRRRDLFDSPCHHFVRLSY GPTLDILARGCDGIERVVRKFQALEAEGAYGVPKAPSPSRTEGEKEPHTVPSAGGGER EKDEELHLL" | VPGGRAGLIRIAAVLNNAYVGFFIPDYTAYNEMLSLEKNFAAIFVPLSEEDDYHIHPE KIAEEIARGTSVIITSNPRNPTGRVVANPELAEIQDICRERATLVSDEFYSGYNYTSN CDGTTISAAENVQDVDEDDVLIIDGLTKRFRLPGWRVAWILGPKEFIKAIGSCGSYLD | /ta-151-031-032 / TEATH OF THE PROPERTY OF THE | /product_scarced hypothetical protein" /prodein_id="CAD21073.1" /protein_id="CAD21073.1" | contains EST gb:AA897847, BG278951, BG279936, AA899026, BG279935" [AGAIN STITE] | otransferase PA4722, | /gene="83H20.010" /gene="83H20.010" join(212322152.2141621461.21521 .21639.21698 22965) | | /chTomosome="6" _feature 118481 | 1122151 /organism="Neurospora crassa" /db xref="taxon:5141" | Location/Qualifiers | Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage groups II | Sequencing was performed by MWG Biotech AG, Ebersberg, Germany, http://www.mwgdna.com | this contig is an assembly of BAC 23H20 from 1 to: 52608, and BAC 22H2 from 52608 to: 122151 (Strain OR74A); BAC clones are available | Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail: G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf, E-mail: ulrich-schulte@uni-duesseldorf.de | Direct Submission Submitted (18-JAN-2002) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, | 2 (bases 1 to 122151) German Neurospora genome, project. | Schulte, U., Aign, V., Hoheisel, J., Brandt, P., Fartmann, B., Holland, R., Nyakatura, G., Mewes, H.W. and Mannhaupt, G. | Sordariales; Sordariaceae; Neurospora. |
| | | CDS | gene | exon | intron | exon | intron | exon | intron | exon | 110101 | intron | exon | intron | | exon | intron | exon | | | CDS | gene |
| | Saccharomyces cerevisiae, PIR:A55428 Contains Multicopper oxidases signatures [GWMLFHCH.EWHMISGLAVTF]; Multicopper_Oxidase2 [HCH.EWHMISGL]" /codon_start=1 /product="related to cell surface ferroxidase" | <pre>complement(join(2795329206,2926730094)) /gene="B23H20.030" /note="similarity to ferroxidase precursor, YMR058W,</pre> | . គ្នា គ្នា | 2558525698 //gene="B23H20.020" /number=7 /27953 20004 | 7.000000000000000000000000000000000000 | /number=5 2544725518 /gene=B23H20.020" | /number=5 25398. 25446 /gene="B23H20.020" | /number=4 25263. 25297 /gene="B23H20.020" | /517825262 /gene="B23H20.020" | 2509725177 /gene=#823H20.020" | Υ.H. | / yette="bz3nz0.020" /number=3 2506325096 | /number=2 2504825062 | 2489125047 /gene="B23H20.020" | ΪB. | /gene="B23H20.020" /number=1 24852 24890 - | /number=1 2420524851 | KQGASAYMFLSANDIEESSEAHGRAAGGSSEPDGQDQRKKGEALKDQTAAALSAEGLA ASLQADNEAMLEAAVPDASPTPGAGTTHKRVRNADSGVGSSVDSI" 2411724204 /gene="R33420 020" | /protein_id="CAD21074.1" /db_xref="G1:18376328" /db_xref="G1:18376328" /translation="WILVEWPHGTTIPESCOASTOCROCGEDARREFERERE | /gene="B33H20.020" /codon_start=1 /product="hypothetical protein" | / yerre="527720,002" join(2417. 24204,2485224890,2504825062,25097. 2526325297,2544725518,2558525698) | 24117 |

| | 0 | |
|---|--|--|
| AGCACCACATGGCTGAGAGGATCGCGGCGGT 1438 | 1408 AG | |
| CCGAGCAGAGGGTCTCCATGGGGAAAAGGGCTATGGCAGGGTGAAGGAAATGTTCATGG 1407 | 1348 CC 13908 AG | |
| CTGCTGGGAAGGGCGTGGCGCCTCTTGCAAAGAACATCGTCAGACTCGCAAGCCACG 1347 | 1288 CTC 13848 ACC | |
| | | |
| GTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTGG 1227 | 1168 GTV 13728 GTV | |
| 3.4%; Score 58.2; DB 8; Length 122151; Similarity 50.9%; Pred. No. 0.079; 18; Conservative 0; Mismatches 133; Indels 0; Gaps 0; | Query Match Best Local Simi Matches 138; | |
| 3344435567 | gene | |
| | exon | |
| /number=1 325732636 //cene-#833490 040# | intron | |
| WPLIPQKTEVEDGSEKGSLFGRLSWRKGRA" 3176532576 /gene="B23H20.040" | exon | |
| MKEKWRGKMIKAMEGKEKNKKKSKGGRVAGGEEDMERGETVERORGWWVKFKAMMERY VMFILPFVTYLREGYEALVFVAGVSFAAPATSIFIPALYGVIYGSLVGVVLYKFGSST KLOLFLVLSTSLLYLVAAGLFSRAIMALESQOMAKAIGSDAVELGSGPGSYDIDKSVW HVDCCSPOVNGGGGMGIFNAIFGWTNSATYGSVIGYDLYWLVVIVSFLVMRYREVXGK | | |
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| /product="related to high-affinity iron permease" /protein.id="GAD21076.1" /db_xref="GI:18376330" | | |
| candida albicans, "KKWB1:AF195//6_1 contains EST gb:AA901925, BF072546" /codon_start=1 | | |
| similarity to high-affinity | | |
| | CDS | |
| 1 3022030243 note="24 bp agtcagtcagtc tandem repeat" 3176533093 | repeat_region | |
| /gene="B23H20.030" /number=2 | | |
| / yeire = party (300 / 1) / number = 1 / number = 1 / complement (2926730094) | exon | |
| /number=1 complement(2920729266) | intron | |
| vvvvvii EXP complement (2795329206) /gene="B23H20.030" | exon | |
| YTHPFILSHNSIVQIVLNNLDSGRHPFHLHGHOPQILHRSGADEGTWSPSSSSSSTS SFSTSNGSNHTAPMRDTLVVEDNGSAVIE RQADNGFWLFEGLEWHHISGLAVTFI EABYLQQTINLPADHLAACRDRODDIPEEGUNAAGRGGKDKNDLSGWLLJLDAQDSPPK PIPAGFTGGGIAALTMSCFTGILGVAVVAWYGFSEPVGESNTAAAMVKTKSPAAAGES GSEGGVYTDVDUDSAGKSASVVRVKRGTEAVESEALSFGSEEEAVNGVGWATSKKGDG VATUUNDA TENDA " | | |
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIZNY, D. M., Adams, C., Adio-Oduola, H., Ali-Sman, F. K., Alien, C., Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Ayvele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bomin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkett, C., Burrell, K.L., Byrd, N.C., Chen, G., Chen, G., Chen, R., Chan, C., Chen, G., Chen, R., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H. H., Delaney, K.R., Delyado, O., Dem, A.L., Ding, Y., Dinh, H. H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K., Earnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Besotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Ganner, T., Garza, N., Gill, R., Gorrell, J.H., Gouvara, M., Gunratune, P., Hale, S., Hamilton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Haber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L., Lichtarge, O., Lieu, C., Liu, T., Liu, M., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, B., Massey, E., Mawhiney, E., McLeod, M. P., Martin, R., Martinde, A., Martinez, S., Mier, G., Metson, J., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nederson, E., Nochenko, S., Ogih, M., Ownoun, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Stocher, S., Stote, B., Shen, H., Shooshtari, N., Sisson, I., Shooshtari, N., Sisson, R., Martinez, B., Williamson, R., Walco, M., Warren, R., Washington, R., Mang, O., Warren, R., Washington, R., Mang, O., Walliamson, R., Marcin, R., Wooden, S., Worley, K., Ward-Moore, S., Mareren, R., Washington, C., Waltington, S., Williamson, A., Tanerisa, A., Tamerisa, K., Tang, H., Thomas, S., Marey, G., Shen, R., Washington, C., Waltington, S., Walter, R., Marinden, S., Wooden, S., Worley, K., Walter, R.
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AC126306.1 GI:21699124
HTG; HTGS PHASE1.
Rattus morvegicus.
Rattus morvegicus
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Direct Submission
Submitted (05-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 152607)
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                                                                                                                                  Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                            Worley, K.C.
Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                      Center: Baylor College of Medicine Center code: BCM
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Center project name: GZIY

Center clone name: CH230-207N13

Center clone name: CH230-207N13

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 92980 bases at least Q40

Consensus quality: 99800 bases at least Q20
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NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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39966

78

138

39906

198

CDS

CDS

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REFERENCE
AUTHORS
TITLE
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AB026653/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Address for correspondence: kaos@kazusa, or.jp
Address for correspondence: kaos@kazusa, or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=NVC8

Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Gene Bencoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39725 CCCGCCCCTCTCCCCGCCCCC 39705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35762
Arabidopsis thaliana genomic
AB026653 BA000014
AB076663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-APR-1999) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 35762)
Sato, S., Nakamura, Y., Kaneko, T., Kato, T., Asamizu, E. and Tabata, S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones
DNA Res. 7 (2), 131-135 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S Structural analysis of Arabidopsis thaliana chromosome 3. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB026653.1
                                                                                                                                                                                                                                                                                                                                                                                  This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MSJ11 and the 3' clone is MSJ1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20277480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTCCTCGTCTCCCATGAGC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTCCCTCTCTGGTGGTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (sites)
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/product="protein kinase-like
/protein_id="BAB02873.1"
                                                                                                           join(2370. .2410,2893.
/note="gene_id:MVC8.1"
                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"
|strain="Columbia"
|db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                    /clone="MVC8"
/clone_lib="Mitsui P1"
                                                                                                                                                                                                                             /chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:4757409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dy dy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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                                                                                                                                               .3389,3462. .4095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLN 27-DEC-2000
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/translation="MKYYSSRRELRTQFYIVNPVTMRWTSIPETHREFSILPIGLSRN
GSKGKYYVKLTATTPSQLKVYVVDSKRGQRKFYCIEHPBWSEGGWPTQCQAVNPNK
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VCYPFPNNHHLISIWTLVDYEQSLWKKEHDGYVFRDWVSGIPWIQDYMRQYYLLETTKQ
MSFLMAVFMDKRAPPETRKRIIFPHPLLCHPNNPLLVYLYLPESIVSLDVATKKLQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGGSVEVPGMAIGVPTLSRSSSVHRSLEPTKKWTMSSVKFVTSF
RNPSNCSGTKRSFRVMASDDRSEQADNCQGIQEDLNYLLKIGVGSVAGAAIIKYGSVL
FPQITRPNLTLALFIIIAPVVISVILLSLSSSSSKKQN"
join(9979. .10477,10563. .11050)
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LGEGRFGSVYWGQLWDGSQIAVKRLKEWSNREEIDFAVEVEILARIRHKNLLSVRGYC
AEQGERLLVYEYMQNLSVSHLHQQHSAECLLDWYKRMKIAISSAQAIAYLHDHATPH
IVHGDVRASNVILLDSEFEARVTDFGYGKLMPDDDTGDGATKAKSNNGYISPECDASGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKKEFVKKSLPQAPPKKILRMRNQTLLEERRCSLEDMMNRLLSDIDISRSALIATFLE
LEAAVRSYFNDEYQETEDYSGDIPSLLPTTISDVPGSSSYTLDHDNISADETSNASTM
KEBANLKNLFSRNSTAVDNYTDWHELITTYSLDVGSSFQEKFELSSTNGDAATGTV
KHDEANLKNLFSRNSTAVDNYTDWHELITEYGLLDQSSPQEKFELLSSTNGDAATGTV
TRGGISGYGGIQRLDGSDRKFQELTIESIKKTHVSDFEASTAVEPDLVNQCAMDLHGE
AHGMYGAVGGDTETQKDLAIVFQSEERHKLKRVIDTLKRRLETAKADTEDLISRLNQ
ELAVRQFLSTKVRDLEVELETTRESCKQCMEKTVLDEKERFTQIQMDMEELRKQCMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(11749. .12006,12087. .12305,12418. .1266
12743. .12907,13038. .13744,13916. .14024,14098. .14184,
14277. .14375,14479. .14589,14667. .14936))
/note="emb_CAA16573.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(4337.
/note="gene_id:MVC8.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESETSDVYSFGILLMVLVSGKRPLERLNPTTTRCITEWVLPLVYERNFGEIVDKRLSE
EHVAEKLKKVVLVGLMCAQTDPDKRPTMSEVVEMLVNESKEKISELEANPLFKNPYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESFLNSIKDEKTHIETANESLVQENQMLLQQINDIRENFENFHKEHEELEVKAKAELK
VLVKEVKSLRTTQSDLRQELSGIMKEKLEMERIVQREKDREETAKNADKKLLHECDVL
QNRLQECNVKFDIEEEGKLIMDSSSLSEAIELLATSDNRIGLLIAETQULSEEVEKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNTSYSHDGANGREPDTDSRASPPHRHDGRSPLPLGMDWSSPPRHLEGRDTVWPHDHR
TGWSYCVTVPSWVDLPKSSVSDPAVFYRVQVAIQSPEGITSARLVLRRFNDFLELYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strong similarity to unknown protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
YIDKNKIKNDVVVGNALIDMYFKCGCSEKAQKVFHDMDQRDKFTWTAMVVGLANNGQG
QEAIKVFFQMQDMSIQPDDITYLGVLSACNHSGMVDQARKFFAKMRSDHRIEPSLVHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene_id:MVC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIDLARTVMSKILEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKDIKRGTCPKVGRYESGYDMVIPMTLHLEPSLLSDHERVLLPCHKRTHVVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                 SWT1M1DGYLRAGCFNESLE1FREMQSAGM1PDEFTMVSVLTACAHLGSLE1GEW1KT
                                                                                                                   ES I ELLVEMERNLVS PTSVTLLLVLSACSKVKDKDLCKRVHEYVSECKTEPSLRLENA
LVNAYAACGEMD I AVR I FRSMKARDVI SWTS I VKGYVERGNLKLARTYFDQMPVRDR I
                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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/db_xref="GI:9294596"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strong similarity to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="gene_id:MVC8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="gb|AAC35225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oin(15425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTSGGHRGTDDLVRKMLTEVLIDNARLRKQVNSVLRCSLSGHGISVREAGTEVDDEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MNLYAHDLSLLDFNYNVSGPFGEPLSHRFLSPGPFFQGEEDDYR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evidence=not_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 id:MVC8.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .17406,17640. .17745)
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                                                        Similarity
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                                                                                                                                                  /traibletion="MGYKFLALGLSLCLVLSSFYQVSCODEGTGSLSTLDLIEHEYQT 
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AAHAGFEQLKTDDSAQGLDDEQSAKRQSMLDEIERDFEATKGLEQLKADDLTGINDE 
EHAAKRQKMLEBIERBFEBATKGLEELHSTSSTDDBAQSAKRQNMLDEIEREFEBAT 
SGLKELKINAHTVKDDVDDKEQDAKRQSMLDAIEREFEAVTESFKQLEDIADNKAEGD 
DESAKRQSMLDBIERBFEBATNSLKQLNLDDFSEGDDSAESARRNSMLBAIEREFEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(25764 ..26471,26569 ..26672,26774 ..26803,
26889 ..26948,27028 ..27060,27161 ..27211,27291 .27335,
27450 ..27497,27584 ..2765,27751 ..27798,27884 ..2735,
28033 ..28082,28174 ..28339,28333 ..28380,28465 ..28539,
28036 ..28683,28773 ..28835,28927 ..28974,29061 ..29126,
28036 ..28683,28773 ..28835,28927 ..28974,29061 ..29126,
28036 ..28633,28773 ..28835,28927 ..28974,29061 ..29126,
29227 ..29274,29369 ..29434,29524 ..29571,29528 ..29732,
29856 ..29253,30039 ..30154,30249 ..30290,30368 ..30422,
30517 ..30591)
                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/evidence=not_experimental
/protein_id="BAB02881.1"
/db_xxef="GI:9294600"
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HNEYNRDADQKVGRCISSVLKRSRVIASII[FIVSTVITSISKLSTTEALKNYI]HFS
NRLIAFGRSSCAPILKTSSMDGIGFNIKICLQVAKKKIAKNSTVQALVVMKRRR"
complement(join(21613. .21855,21947. .22003,22111. .22946,
23211. .24168))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(20658. .21062,21115. .21180))
/note="gene_id:MVC8.7
/nknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/product="glycosyl transferases-like protein"
/protein_id="BAB02880.1"
/db_xref="GI:9294599"
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/evidence=not_experimental
/protein_id="BAB02879.1"
/db_xref="GI:9294598"
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/note="emb|CAB10501.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="gene_id:MVC8.9"
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/protein_id="BAB02878.1"
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KSHLQSEBIYMKLEELAQESTFAAYLFDTSELLFEAGNKELEEHSQVTTLRTNPIESI
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            0,
        Score 56.4; DB 8;
Pred. No. 0.17;
0; Mismatches 101;
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            101;
                                                                                 Length 35762;
    0;
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AF128457
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AF128457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-FEB-1999) Waksman Institute, Rutgers University, 190 Frelinghuysen Rd., Piscataway, NJ 08854-8020, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Oryza sativa (indica cultivar-group)
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Oryza sativa subsp. indica BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF128457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCATCCTGCTGGGAAGGAGGGCGTGGCGCCTCTTGCAAAGAACATCGTCAGACTCGCA 1340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAAACCCATCTACAAGGCTACAACTAGGTAGCCAAGGACGTGAAATCGTTGAGAAGATG 21676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 70311)
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/trānslation="MDGEQEARWLAAQGVAVGADLVAAALRQLEFLAAVDRRRWLYEG FLLERAHIREVILKWCIFQVQYLKDCKRLYGRILDNSNVESSIRAESKHAGEKVWAEQ YPKPFFELENTSSSDNSITYANAGAAEDISYDLWHAHSKOSSDNSITYANAGAEDISYDLWHAYKRQSETYGHDMLKLIGREVLE EALARYKGFLYLIKTNQENKMKLFRYPTYDVDVMHSKGHQLHPATYCHDMLKLIGREVLE HDDTDDDRSEGKKLDTGFESGTTEQFENAFGARYWKAGAMYRGNLPSPVTSNPQMFSGE VNGEFSVGKAESQITILETTVIELFLQIVDIKNLPPAIFKENVYIWFTKNQPDMFISD
                                                                                                                                                                                                                                                                                     join(<2846. .3003,4043. .4325,4560. .5015,5301. .5833, 6229. .6424,6527. .6685,6334. .>7670)
/product="hypothetical protein"
join(2846. .3003,4043. .4325,4560. .5015,5301. .5833, 6229. .6424,6527. .6685,6834. .7670)
/note="similar to Oryza Bativa EST clones S1328 1A found in GenBank Accession Number D39744 and 96BS0679 found in GenBank Accession Number AA753512"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      putative map location based on mapping of Oryza sativa EST clone E10310 6Z found in GenBank Accession Number C99155" join(162. .367,452. .>556) /note="predicted gene - truncated (3'); similar to Oryza sativa EST clone 97AS2194 found in GenBank Accession Number AA753140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
                                                                                                                                                                         /product="hypothetical protein"
/protein_id="AAD27627.1"
/db_xref="GI:4680336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="php20725 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Teging"
/sub_species="indica"
/db_xref="taxon:39946"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lou, A., Young, S. and Messing, J. inearity in cereal genomes
                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="16F19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lou, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Young, S. and Messing, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone 16F19 php20725 region,
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| inthar_redar | , | repeat_region | repeat_region | repeat_region | repeat_region | repeat region | | | CDS | mRNA | | | | | C | CT . | mRNA | | | | | ; | CDS | mRNA | repeat_region | repeat_region | repeat_region | | | | | |
|--|------------------------------------|--|---|--|---|--|---|--|---|---|--|--|--|--|---|---|--|---|--|---|---|--|---|---|---|---|--|--|---|--|--|--|
| /rpt_type=dispersed | ~ | /rpt_remily="purative milk h" /rpt_type=dispersed 2416724475 | METE | type=dispersed lement(2054620624) | /rpt_family="putative MITE B" /rpt_type=dispersed 20325 20653 | LSRSWILITILAGTHYDMLRPSLSDPPLPRLVAHRTTSLVPFAVPPHSAWVLNVAGPDH RHHRPEGPPSPTSPRCSSTPSPFSSGILTVEEKR" 1980119945 | /translation="mwaswstdecakrrtrrgggrgrgvgggggggaagklllspnps sltppppreeggggergvggmehhlactakrrtrrgggrgrgvgatiig;wmrhpsarl prhtphytyatu | /product="hypothetical protein" /protein_id="AAD27635.1" /db xref="GI:4680344" | <pre>join(1607216311,1631616834) /codon_start=1</pre> | join(<1607216311,16316>16834) /product="hypothetical protein" | RDADGHIDCHTHAAQERAEQLANFQLFGLVFLVCAYALGCFAVAAARHGHPDLATWHA KHVAAMEAOLAGAGAGEGDRFVGSALFLEDTAI" | MLIMFFLFGITALLSQKTRYLDI. DEGALCLIVASTAFMABILLLFYFHSTTHQGLBGYYH YLLVVVVALCVATTVIGALLPASFPVDI ASGAATALQGLWFYQTAFTLYGPSLPAGCR | / WGSFGAPAWI-PAHI-PI-VVI ACCAFT HMCVFVI-VS-THILH TEADGGTNPAHLNDLEHGG | /product="nypornetical protein" /protein_id="AAD27628.1" /Ah vref=md1.4680137" | /codon_start=1 | /product="hypothetical protein" | RHGHPDLATWHAKHVAAWEAQLAGAGAGEGDRFVGSALFLEDTAI" join(<1147511836,13787>14354) | STTHOGLEGYYHYLLVVVVALCVATTVLGALLPASEPUDIASGAAIALQGLMFYQTAF TLYGPSLPAGCRRDADGHLDCTTHAAOERABOLANFOLFGLVFLVCAYALGCFAVAAA | PRGFRLRAMNPUDVGGGGAPAMLPAHLELYVIAGGAFLEMCUSVLYSTHLHLFADGGI PRGFRLRAMNPUDVGGGGAPAMLPAHLELYVIAGGAFLEMCUSVLYSTHLHLFADGGI NPAHLNDLEHGGMLLMFFLFGILALLSOKTRYLPIDEGALCLVASTAFMAELLLFYFH | /translation="MQLVSIPEQRERPIKVIKPTASADPARLLQLARPHPSFTLHRTA /translation="MQLVSIPEQRERPIKVIKPTASADPARLLQLARPHPSFTLHRTA | /protein_id="AAD27637.1" /protein_id="AAD27637.1" /db_xref="GI.4680346" | /codon_start=1 /product="hypothetical protein" | al protein" 149011836.13787 | type=dispersed (<1069110915,11490. | / PDT Cype-Cutagerson 10318. 10483 /rnt family="nutative MITE A" | 140 - 150 - 141 - 150 - | 79238069 /rpt_family="putative MITE A" /rpt_type=dispersed | | LTGGAMAQKDA 18EPDYRAMATSAETVAAFFANCGTCGTACGSMAGJUK VAAAKCKAA RCKAVAAGGGGQTESAGCGSGCGGGGGGGGGGCAKVVERTKAGGGGGGGGGGKSGGC GSGCGGGGGGAMVVESSKDDVHAKSAGCGSGCGGGCGGGCGGGMVMBSSKAAHV | DNKWSISSSNICTTRUMKESKUGSTEIMKEDWFLLPWIVLSFWSQDINVKDGEKLI SATTAVKFSAEYPYGKAVALLDTKSELIMVKEDWFLLPWIVLSFWSQDINVKDGEKLI | SKLSFERWELKEHDGHASSTEVS VKVAASSTEVFVKAQQVUSTIKLIBEF SLASIISEN SVKDQKMSCWTRFVYDCHTELIRQIRDKKAKMOWVARELVGUTKSSKKPFKLAEFV SVKDQKMSCWTRFVYDCHTELIRQIRDKKAKMIN VEGETA | GGRLDISTKTGKSIGASIOCEPTGELILTÝLVDRTSSSKKPKKIGKVSVSLQEFTWSD |
| repeat_region | LTR | repeat_region | | | | CDS | mRNA | repeat_region | LTR | repeat_region | | repeat_region | repeat_region | | - | | | CDS | mRNA | | misc feature | stem_loop repeat region | | | | | | | | | CDS | mRNA |
| complement (4786848017) /rpt_family="putative MITE C" | 4714947522 /note="putative LTR" | | RRGAGASQTGVGGAADAPLNRPKVFLIYQCSDPWRHAAYALSYÄQHASSIGTLNSAAP RRGAGASQTGMPEPSSPPPHQRQPPPPPPPRRQPPPPSSPRRIVAEYTNNDIDDVII ******************************** | / LIGHS LIGHT PROLIFERING HEART DESPONDED DE LA CHARLES DE | /product="hypothetical procein" /protein_de"aAb27633.1" /db_xref="GI:4680342" /db_xref="GI:4680342" | /product="hypothetical protein" join(4539345921,4647946533,4738247453,4745847671) /codon_start=1 | <pre>/rpt type=dispersed join(<4539345921,4647946533,4738247453, 47458>47671)</pre> | /note="putative LIK" 43355. 43549 /rpt family="putative MITE D" | /rpt_type=dispersed 4190742271 | complement (4135141471) /rpt_family="putative MITE B" | <pre>/rpt_family="putative MITE B" /rpt_type=dispersed</pre> | /rpt_type=dispersed 4095741072 | 3963739788 /rpt family="putative MITE C" | RRILIDRE PERSOPERELAAASSATASASRTGCGRLVRDHLRLHTWPPPPLVRDCHRSS TARLRIR LSSACADELLRPHARHSL" | LITPCAGEPTLFGGEVEPACCAQLRAQAACLCAYARSENYGSYIRSENAKRLFTVCGLP | <pre>/db_xref="GI:4680343" /translation="MRKSPPSTSPVYAAAAVLLLMYLMAMGVGVVEAAVLPPSRCNPT</pre> | /product="hypothetical protein" /protein_id="AAD27634.1" | complement(join(3911239523,4203642349)) /codon_start=1 | <pre>complement(join(<3911239523,42036>42349)) /product="hypothetical protein"</pre> | <pre>/note="similar to Oryza sativa receptor kinase-like protein gene found in GenBank Accession Number U72724"</pre> | <pre>/rpt type=dispersed 35968 .37755</pre> | 2589326223 3534035604 | GAGAAAQRAALSARSDVYCLGIVLLELVIGKFPSQYLLTARGGIDVVQWAASAVAGGI EQEVVDPVVAAGAGPAAVRLLRVGVRCTIPEPESRPSMADVARMVEQVAGGGAS" | ARKKSSSSPSDQSPDRVVLDWPARMRIAVGVVRGLSYLHEKLGIPAMRLVSMTGADFD APPPPPHGNLKSGNILLDAHLEPRIVDYGFFPLVNTSQAPHAMFAFRSPEAASAAGA | AĀGAASAQLVTMEQGGSGGGVGGVGGARKQVAEFVLMSNAAGEFGLPELMKASAEVL GNGTLGSAYKAAMRNGVTVAVKRMRDMNRVGRAEFEEHIRMLGELRTPTSSPPSATIT | RLTGVLPEAVAARFNESAFAGNPGLCGAPGSGAGACAAAAPGPAHSAMPPMSAADYFA VORETSVFVVMGIIMLVVLLVAGAMVLMLRODEGTSTASSGYEHPAIGAPSGNLSVPH | EDEPALISKLYGLES INLIKNIESGELPASIAAVESLEALYLISKINAESGEVEDVEAN SMLKKLYLDRNNESGELPAGATAGAPRLQELHLDHNRIEGRVPSKLPATLRLENVSHN | /db_xref="G1'4680345" /translation="myvilliapristlflilliaaga!avdpdgaaapdtaaapdtea avitetaatithetmatemmasessesenoorraffwedvooynguttg!r!arinisgd | / COMUNIT_SCRIPT-1 /product="putative receptor kinase" /protein_id="AAD27636.1" | GenBank Accession Number C73087" | /product principle 1.58820,2647227849)) complement(join(2516225820,2647227849)) /note-"gimlar to Oryza sativa EST clone E2886 2A found in | <pre>complement(join(<2516225820,26472>27849)) /product="mutative receptor kinase"</pre> |

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JOURNAL
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AUTHORS
TITLE
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Submitted (10-JAN-1999) Waksman Institute, Rutgers University, Submitted (10-JAN-1999) Waksman Institute, Rutgers (10-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhattoideae; Oryzeae; Oryza.
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AF119222
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Llaca, V., Lou, A., Young, S. and Messing, J.
Microsynteny in a gene-dense region in maize,
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complement(690..1043)
/note="similar to Oryza sativa EST
GenBank Accession Number D23571"
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                                                                                                                                                                                   /note="similar to Oryza sativa EST
GenBank Accession Number AA753140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MEGDSFSGMANGGQVDNKLIQTFHKSFVQVQSILDQNRMLINEI
NQNHESBAPDNLTRNVGLIRELNNNIRRVVGLYADLSASFARTMDASSEGDSSGTLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (<690.
                                                                                                                                                                                                                                                                          join(<3234. .3341,5600. .5844,6446.

/product="hypothetical protein"

/poin(3234. .3341,5600. .5844,6446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lou, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="hypo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to the Zea mays php20725 (PIO20725) on chromosome 4; similar to Sorghum bicolor group complement(<690. .>1043)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:39947"
/clone="BAC 1.H19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
variety="japonica-lemont"
                                                                                                                                                                                                                                                                                                                                                                           oin(<3234. .3341,5600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="Clemson Lemont"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young, S. and Messing, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 8
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8; Length 70311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                         .6651,7318. .7478)
clone 97AS2194 found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone
                                                                                                                                                                                                                                                                                                                                                                 .6651,7318. .>7478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sorghum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C3025_1A found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLN 26-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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repeat_region
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YDLVAAVKRQSSFFYQVDTPTMHDQRFLEEALARYKGFLYLIKTNQENGWKLFRVPTY
DVDVIMHTHQLHPATYCHDMLKLIGRVLEHDDTDDDRSEGKKLDTGFSGTTKQFENAP
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SSTVPVKAQQVLSMIRTEPFSLSKEFLSPNSISHLGTTWAWSGNSULCITNDKPSKDGSILELK
CDNKTIKLYGGKRLEFQDINVEDGSKLIGGASIAQKGAISBPDTAAMATSAETVAAP
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CDNKTIKLYGGKRLEFQDINVEDGSKLIGGAIAQKGAISBPDTAAMATSAETVAAP
NCGTCGTAGGSMWAGDKVVAAARCKAARCKAVAASGGGGGCGGAGAMSESKADVHAKCAGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                            MLLMFFLFGILALLSQKTRYLPLPEGALCLVASTAFMAELLLFYFHSTTHQGLEGYYH
YLLVVVVALCVATTVLGALLPASFPVDIASGAAIALQGLWFYQTAFTLYGPSLPAGCR
RDADGHIDCHTHAAQERAEQLANFQLFGLVFLVCAYALGCFAVAAARHGHPDLATMHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IETSNHIILRCKLAGEVWKKLNLYETAVRSSNIQDFVESILDTLPEHQKPGWPACFAA
CSHGLWKARNQLIFKLTETSVAYILHRIRESLQLWVHRLKPSLREHLNTWADKLS"
join(<19445. .19806,21796. .>22363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(<14851. .>15846)
/product="putative reverse transcriptase"
complement(14851. .15846)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JULIN (*9366. .9523,10351. .10468,10600. .10851,11086. .11541, 11831. .12363,12718. .12913,13018. .13176,13330. .>14262) /product="hypothetical protein" join 19366. .9523,10381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGCGGGCGGGGCGAMLNAST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(9366. 9523,10351. .10468,10600. .10851,11086. .11541, 11831. .12363,12718. .12913,13018. .13176,13330. .14262) [1831. .12363,12718. .12913,13018. .13176,13330. .14262) [note="similar to Oryza sativa EST clone S1328 1A found in GenBank Accession Number D39744 and Caenorhabditis elegans protein encoded by GenBank Accession Number AF003148"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein"
join(19445. .19806,21796. .2236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MGEEKGGFIRGSSSWGKGQLSFLGGRPARATGRTSQGAFQTAGQ
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LFPAGGGGGFLSPATCSSATRHLEQEETTLLKGGDVADGEMRADGEARRKHRRRRRRR
                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                        oin(24077. .24316,24321. .24839)
                                                                                                                                                                                                                                                         product="hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAEPPRHGQLLHRRRRGLHRRRPRRVFASKRFSCTIDSVLEYTDECSLIFCTTAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon start=1
                                                                                                                                                                                                                                                         protein"
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mRNA

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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRN2
                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(30165..30488)
complement(join(431774..32072,32911..>33076))
/producte_hypothetical protein
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TGVLPEAVAARTRUSAFATGAAAPGCAFTAAAPTAAAPTAAAG
EETSVFVVMGIIMLVVLLVAGAMVLMLRQDEGTSTASSGTPPLGAPLRAICAFTHAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAASAQIVTMEQGGSGAAGGAGGVGGVGGARKQVAEFVLMSNAAGEFGLPELMKASAE
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HYRKEEKILVSEFMPRGSLLYVLHGYKSF"
complement (join(42779. 42931,43886. 44595,45422. 45637,
45851. 45988,46130. 46266,47466. 47502,48912. 49126,
52727. 53003,53024. .>53135))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="receptor kinase-like protein" complement(join(40016. .40032,40110. .40588,40596. .41539)) /note="similar to Oryza sativa EST clone E2886_2A found in GenBank Accession Number C73087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MLFQAARQPTAYLNSSEYSSDKRTIWHMYSMLLGALAHRSSSEF RLOPSRERLQWAYPFKTGSLWHSCWFYTVLVGLVHHNLEEVOLFKSATDMAIGDVSW LSRDQIERLAMLIDRGPAIRGGEPHHSRVHGVVVIVCVVAHSIHLLVVLAL" join(<34690. .34730,35085. .35261,35329. .35549,38631. .>39499)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LALRRRRFPMPPATGGERLWWVSPEFREELIAAELAAAVFDASQDKFVECQAMIAEK
RHPEHGYAVVEETSEVMTTICRAFFGRYNESDDDDDDLLCDCVDANECKCGGDDWAN
EFIDEEDDDCSBDVDEEEEKDESCCQRMIYRLR"
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/db_xref="GI:4880493"
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RAIPLPPAIAARSKLASPRYRRGTGAPSFRRGAGAARIIPSVEPASDRPNGHGRSSNY
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complement(join(42779. 42931,43886. 44595,45422.
45851. 45988,46130. 46266,47466. 47502,48912. ...
52727. .53003,53024. .53135))
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ESGSAAGESESESDSDDLDEVIADILEGGDDGGSADYYTGPLLPEGTMLLTKTLVDKI
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join(34690. .34730,35085. .35261,35329. .35549,38631. .39499)
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PSLYVEPALLVEYLLESBERWLVSDGKISBARTSLQWLRGKDDVSDRSAGEIALIADGMU
MITETAVGGHAVGAVRSQSFLGTSTNQMSRHSTEYWHLSDPLVDLGSIHESMSBLGA
GRNGYFEVENISTRJUTEGG/TSGDRGNDSLQGSREAYSAEBGNNDDNLQASLLSQVASA
ETNDINTSFTSBGSSSYLRRHGTSTSGLAQDLISSLHDHDIEEDDEEIHIAALSSQPA

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                                                           ATCTTCGCCGACGGCGCATCAACCCCGCCCACCTCAACGACCTCGAGCACGGCGCGCATG 19753
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Scoring table: Sequence: Perfect score: Title:

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Pred. No. 2.2e-156;
2; Mismatches 382;
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                       WPI;
                                                                                                                                                                                                                             plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                                                                                                                                                                                              Plant microsatellite marker #101.
                                                                                                                                                                                                                                                                                                                               AAA31140;
                                               Havukkala
                                                                      (GENE-)
                                                                                                                                25-JUN-1999;
                                                                                                                                                         29-DEC-1999
                                                                                                                                                                                WO9967421-A1
                                                                                                                                                                                                       Eucalyptus grandis
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                                                                                                          25-JUN-1998;
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                       2000-116958/10
                                                                      GENESIS RES & DEV CORP LID & FLETCHER FLETCHER CHALLENGE FORESTS LID.
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New plant microsatellite markers and associated flanking species

for

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RESULT 3
AAZ93717
ID AAZ93717
AC AAZ9
AC AAZ9
AC AAZ9
AC AAZ9
XX Ubiq
KW Ubiq
KW Ubiq
KW dest
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KW oncc
KW ss.
CXX Synt
CXX Synt
CXX Herr
AXX WO20
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PR 009-C
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Best Local Sim
Matches 196;
                  Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                  Ubiquitin ligase; SCF; F-box protein; targeted degradation; destabilisation; proteolysis; drug discovery; gene therapy; cancer; oncoprotein; Huntington's disease; gene knockout; delivery systems;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAA31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and dlibrary screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes.
                                                                                                                  09-OCT-1998;
                                                                                                                                                               08-OCT-1999;
                                                                                                                                                                                                                                                               WO200022110-A2
                                                               (HARD )
                                                                                                                                                                                                                  20-APR-2000.
                                                                                                                                                                                                                                                                                                               Herpes
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                  Howley P;
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Pred. No. 1.8e-33;
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Best Local Similarity 47.6%;
Matches 147; Conservative
Barley; alpha amylase leader sequence; plant expression; organophosphorus hydrolase; OPH; environmental detoxification;
                                                                          Optimised nucleotide
                                                                                                                                                                                                                          AAZ30007 standard; DNA;
                                                                                                                             26-JAN-2000
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912 BP; 149 A; 353 C; 289 G; 121 T; 0 other;

DB 21;

0;

Indels Length

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The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin Cligases) which can be used for the targetted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of the target polypeptide and thereby recruiting the target polypeptide concerning and thereby recruiting the target polypeptide to the ubiquitin ligase. Such methods are useful for decreasing or increasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Degrading any desired protein in a cell is useful for preventing or treating diseases caused by the presence of abnormal amount of the specific polypeptides, for drug discovery and conceptoteins, Huntington's disease, other proliferative disorders and conceptoteins. The method provides a quick and easy also include an concepton development in the method provides and the development in the method provides disorders and concepton development in the concepton development development
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303
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 CIGGCGGCC
                                                                                                                                                                                                                                                                                     CTCGTCTCC
                                                            CCATGGACCCCCCGGGTGGCCGGCTTTAACAAGCGCGTCTTCTGCGCCGCGGTCGGGCGC
                                                                                             CTCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTC
                                                                                                                             CCCGCGCAGGGGCTGGCCAGAAAGCTGCACTTTAGCACCGCCCCCCAAACCCCGACGCG
                                                                                                                                                           GGGTTCCTCCTCCGCGGTGCCCTGCGAGACCCTTGCGACGGCCGTGGGGGACCCCGCCCCCC
                                                                                                                                                                                             CCAGAATCCGCCGCACTCCCAGACGCCCCCGCGTCGACGCCCAACCCGATCCAAGACA
                                                                                                                                                                                                                            AACCGGACCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCA
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633
                                311
                                                                                                                                                                                                                                                                                                                                                                                           Score 49.8; DB 2
Pred. No. 0.0018;
0; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                           162;
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(first

entry]

1076

ВP

sequence encoding organophosphorus hydrolase.

196 TCGGCTCCCGCAAG 209

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Query Match
Best Local S
Matches 103
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Pseudomonas dimin
Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an optimised nucleotide sequence encoding an organophosphorus hydrolase (OPH) protein atached to an optimised sequence barley alpha amylase sequence. The products and constructs can be used for environmental and in situ detoxification comprising exposing contaminated material to OPH, or detoxification of organophosphorus neurotoxin contaminated soil. The products can also be used as agricultural and domestic pesticides, including insecticides, fungicides and herbicides or chemical warfare agents. The OPH can also be used to hydrolyze other chemical agents or compound containing P-O, p-S, P-CN and P-S bonds. The products can be used to produce transgenic plants which are capable of expressing OPH at levels greater than that of the typical 10-15mg/l of E. coli or baculovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleotide sequence, used to detoxify organophosphorus compounds used as e.g. insecticides, fungicides, herbicides or chemical warfare agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jilka JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1999;
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insecticide; fungicide; herbicide; chemical warfare; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Fig 4A-B; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agents
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1076 BP; 149
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TCGTCTCCCATGAG 317
                                                                                               TCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGTTCATGAGGGTCCAAGCTCGTGCTCC 303
                                                                                                                                                                                         GGTTCCTCCTCCGCGGTGCCTGCGAGACCCTTGCGACGGCCGTGGGGACCCCGCCGCCC 243
                                                                                                                                                    CCGGCGACCGCATCAACACCGTGCGCGGCCCGATCACCATCTCCGAGGCCGGCTTCACCC
                                                                                                                                                                                                                                       ACCGGACCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCAG 183
                                                                   TCACCCACGAGCACATCTGCGGCTCCTCCGCCGGCTTCCTCCGCGCCTGGCCGGAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diminuta
                                                                                                                                                                                                                                                                                                                           Conservative
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/*tag= (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Pseudomonas diminuta organophosphorus
hydrolase sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "barley alpha amylase sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                           2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                          A; 484
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                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                         Score 48.4; Di
Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          C; 276 G; 167 T; 0
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S 망 Ś 닭 5

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for improving the recovery of an active enzyme from a plant where the enzyme requires a transitional metal cofactor for activity. The method comprises introducing into the plant nucleotide sequences encoding the enzyme and exposing the enzyme to the metal cofactor. The method is useful for improving recovery of active enzyme which requires a transitional metal cofactor for activity, preferably for improving recovery of active laccase which requires copper for activity. The method can be used for improving recovery of active organophosphate hydrolase (OPH, E.C. 3.1.8.1) which requires zinc, nickel, cobalt or manganese for activity, where the method further comprises adding bicarbonate ion salt. The present sequence encodes OPH isolated from Flavobacterium sp., which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Organophosphate hydrolase; enzyme; dimeric metaloenzyme; metal cofactor; gene; plant; E.C. 3.1.8.1; zinc; cobalt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Organophosphate hydrolase gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Fig 20; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Improving recovery of active enzyme e.g. laccase, which requires transitional metal cofactor e.g. copper for activity, from a plant, by introducing plant nucleotide sequences encoding the enzyme and exposing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hood E,
Woodard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROD-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1082 BP; 151 A; 484 C; 278 G; 169 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                it to cofactor
                                                                                                                                                                                                                                                                                                                                                                                 Local
136
                                                                                                                                                                                                                                                                          184
                                                      244 TCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTCC 303
                                                                                                                                                                                                                                                                                                                                                          103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Howard JA,
                                                                                                                                                                   gerrecreceres are consequent of the second control of the second c
TCACCCACGAGCACCTCTGCGGCTCCTCCGGCGCTTCCTCCGCGCCTGGCCGGAGTTCT
                                                                                                                   CCGGCGACCGCATCAACACCGTGCGCGGCCCGATCACCATCTCCGAGGCCGGCTTCACCC
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                                                                                                                                                                                                                                                                                                                                                                                 2.8%;
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                                                                                                                                                                                                                                                                                                                                                    Score 48.4; D
Pred. No. 0.00
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       0049
                                                                                                                                                                                                                                                                                                                                                                                                              DB 24;
                                                                                                                                                                                                                                                                                                                                                       91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang
                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 6
AAZ19784
            This sequence represents DNA encoding a Herpes simplex virus type 1 (CC (HSV-1) VP22 tegument protein, which is involved in transcellular CC localisation. VP22 can be fused to cytochrome P450 reductase (P450R) CC (AAY42288). This enables the fusion protein to be delivered to reighbouring cells where it is then transported to the nucleus. Many CC where P450R normally functions. P450R or its derivatives can be used to growing is useful where the active form via reduction. Administration of a crivate prodrugs to their active form via reduction. Administration of a growing is useful where the active drug may be metabolised before it creaches its site of action or where the active drug is cytocoxic, e.g., anticancer drugs. Targetted delivery of such prodrug activators allows a reduction in dose of the prodrug, and thus of systemic side-effects. CC patchiam dose of the prodrug, and thus of systemic side-effects and muscular dystrophy, but may also be used to treat many other conditions associated with hypoxia, ischaemia or hypoglycemia, or to deliver antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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19-AUG-1998;
29-JAN-1999;
                                                                                                                                                                                                                                                                                                            New prodrug activating agent targeted to selected cells particularly hypoxic cells, for treating e.g. tumors -
                                                                                                                                                                                                                                                                                   Example 7; Fig 3; 187pp; English
                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-551046/46
P-PSDB; AAY42292.
                                                                                                                                                                                                                                                                                                                                                                                                  Mitrophanous K;
                                                                                                                                                                                                                                                                                                                                                                                                                   Stratford IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome; nucleus; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpes simplex virus type 1 (HSV-1) VP22 DNA.
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 agents, analgesics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGGCTCCCGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                Patterson AV,
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98GB-0018103.
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/*tag= b
750..751
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Apparent 50 bp deletion between these bases
which alters the reading frame"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       localisation; cancer; tumour; prodrug; reduction;
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poglycemia, or to deliver antibiotics,
anaesthetics, anti-inflammatories,
                                                                                                                                                                                                                                                                                                                                                                                                             Kingsman
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RESULT 7
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Matches 146;
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                                                  06-MAR-1998;
19-AUG-1998;
29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodrug, localization domain; tumor-selective antibody; cytochrome P450; prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor inflammation; atherosclerosis; muscular dystrophy; cerebral malaria; rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; VP22; HSV;
                                                                                                                                                                   05-MAR-1999;
                                                                                                                                                                                                                     10-SEP-1999.
                                                                                                                                                                                                                                                                           WO9945126-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpes simplex virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tegument protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSV-1 tegument protein VP22 encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ07807 standard; DNA; 856 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antineoplastic agents and diagnostic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGACTAAGGCCCCCGCGGCGGCGGCGGGAGACCACCCGCGGCAGGAAATCGGCCCAG
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ilarity 47.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                  98GB-0004841.
98GB-0018103.
99GB-0002081.
                                                                                                                                                                                                                                                                                /*tag= a
//transl_except= (pos:751..754, aa:Leu, Leu, Gln,
//transl_except= Arg, Ala, Asn, Glu, Leu, Val, Asn,
// Pro, Asp, Val, Gln, Asp, Val)
//note= "a line of DNA sequence is possibly missing;
// the corresponding protein has 17 amino acid
// residues respective to this region for which
a DNA sequence of only 4 basepairs is indicated"
                                                                                                                                                                99WO-GB00672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           630
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Pred. No. 0.00
0; Mismatches
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(OXFO-) OXFORD

BIOMEDICA UK LTD

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RESULT 8
AAA29395
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AC AAA2
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AC 12-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%;
Best Local Similarity 47.2%;
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides a new prodrug activating agent that comprises: (i a localization domain (LD; other than a tumor-selective antibody) and a prodrug activating domain (PAD); (ii) at least one nucleic acid encoding a cytochrome P450 and under control of at least one constitutive or inducible expression control sequence or (iii) a modified hematopoisetic stem cell (MHSC) containing at least one nucleic acid encoding a PAD and under control of elements as in (ii). The prodrug activating agent or vectors that express them, are specifically used to treat tumors, inflammation, atherosclerosis and muscular dystrophy, but may also be used to treat many other conditions, e.g. cerebral malaria, rheumatoid arthritis, or conditions associated with hypoxia, hypoglycemia or ischemia, or to deliver antibiotics, antiviral agents, analgesics, ancesthetics, anti-inflammator-ies antibiotics anteriacidation and algents and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anesthetics, anti-inflammatories; antineoplastic agents and diagnostic agents. LD optimize activity of PAD, eg. by delivering it to selected locations or by delivering it to neighboring cells (bystander effect), and allow a reduction in dose of prodrug, and thus of systemic side effects. Nucleic acids encoding the agent may be expressed selectively in hypoxic cells. The present sequence represents a DNA encoding the HSV-1 tegument protein VP22 (complement sequence 106391 to 105486 of genBank sequence X14112). This is used in the construction of a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stratford IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New prodrug activating agent targeted to selected cells particularly hypoxic cells, for treating e.g. tumors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 856 BP; 137 A; 339 C; 270 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Fig 3D; 149pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protien comprising VP22 and a human P450 reductase derivative alP450R
                                   12-SEP-2000
                                                                                                   AAA29395;
                                                                                                                                                               AAA29395 standard;
                                                                                                                                                                                                                                                                                                                                                                                       303
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                                                                                                                                                                                                                                                                                                                              CIGGCGGCC 630
                                                                                                                                                                                                                                                                                                                                                                                          CTCGTCTCC 311
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                                   (first entry)
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                                                                                                                                                               DNA; 900
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                                                                                                                                                               ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48.2;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffiths L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or tissues, inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span; retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis; proliferation; immortal; tumour therapy; macular degeneration; activator; INK4; HSV-1; VP22; fusion protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herpes simplex virus 1.
                                                                                                                                                                                                                                                          New method for increasing the proliferative capacity of cell lines comprises administering agents reversibly activating telomerase activity and reversibly inactivating Rb/INk4 and/or p53 pathways useful in treating age related diseases
                                                                                                                                                                                                                                                                                                                             Hannon GJ,
                                                                                                                                                                                                                                                                                                                                                              25-NOV-1998;
17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200031238-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSV-1 VP22 polypeptide coding sequence
                                                                                                                                                                                                                                                                                                     P-PSDB; AAY96574.
                                                                                                                                                                                                                                                                                                                                             (GENE-) GENETICA INC.
                                                                                                                                                                                                                                                                                                              2000-400055/34.
                                                                                                                                                                                                                                                                                                                             Beach DH;
                                                                                                                                                                                                                                                                                                                                                             98US-0109891.
99US-0120549.
                                                                                                                                                                                                                                                                                                                                                                                       99WO-US27907
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= VP22
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..894
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Disclosure; Page 31; 123pp; English.

The HSV-1 VP22 polypeptide can be fused to a retinoblastoma (Rb) contrivator protein sequence to aid targeting and internalization. The invention concerns methods and reagents for extending the life-span, ce g. the number of mitotic divisions, of a cell. The method relies on cactivation of a telomerase activity and inhibition of one or both of a cRb/INK4 pathway or a p53 pathway. Phosphorylation of Rb by CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the CV cyclin-dependent kinases, cdk4 and cdk6, releases the cells and cyclin-dependent and of growth and differentiation. Long lived (immortal) ceris of use in the production of normal or genetically engineered products.

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Sequence
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BP; 144 A; 354 C; 282 G; 120 T; 0 other;
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               5
                                                       Similarity
 TCCGGAGGGCCGGACGCACCCACCACCACCGCCCCGGGCCCCCGAACCCAGCGGGTG
                 TCGGCTCGAGTTTGATCCGAGCCCACAGTCTCTCCCTCGGGCCCACCGGCGTCCGACCGGCG 62
                                                     2.8%;
                                            0;
                                     Pred. No. 0.00
0; Mismatches
                                                     Score 48.2; DB 21;
Pred. No. 0.0051;
                                             163;
                                              Indels
                                                                Length
                                                                    900;
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                                              Gaps
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RESULT 9
ANAZIGAZ7
ID AAX2
XX AAX2
AC AAX2
AC AAX2
XX AAX2
AC COCL
RW CCCL
RW WO99
XX Huma
RX WO99
XX Huma
RX WPI;
PH COCL
RW WPI;
PH Gift
PT Fusi
PT Fusi
PT Fusi
PT Fusi
PT Fusi
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The invention relates to novel inhibitors of cyclin-dependent kinases (CDKs), particularly (CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells, (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are
                                                                                                                                                                                                                                                                                                                                                                                Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancer fibrosis and neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
                                                                                                                                                                                                                                                                                                                       Example 2; Page 26; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-153770/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1998;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 146;
                                                                                                                                                                                                                                                                Papillomavirus; PV; infection; cell proliferation; E2; peptidomi E1; antiviral; virucide; cytostatic; antiproliferative; dermatol preneoplastic lesion; neoplastic lesion; outaneous lesion; wart; epidermodysplasia verruciformis; anorectal carcinoma; ss.
                           WPI; 2000-171001/15.
P-PSDB; AAY79877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acids encoding a fusion protein (FP) containing: (i) a therapeutic polypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular polypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and a TCP. See AAX26220 for detailed uses of the recombinant transfection system. The CKI polypeptides are engineered to include any of the peptides shown in AAW95097-100 encoded by the DNA sequences AAX26225-228.
                                                                                                                          02-JUL-1998;
                                                                                                                                                      02-JUL-1999;
                                                                                                                                                                                   13-JAN-2000
                                                                                                                                                                                                             WO200001720-A2
                                                                                                                                                                                                                                        Herpes simplex virus type 1.
                                                                                                                                                                                                                                                                                                                                    HSV-1 VP22 peptide encoding nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2000
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                                                                                               (HARD ) HARVARD COLLEGE
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                                                                  Benson J,
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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47.2%;
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Pred. No. 0.00
0; Mismatches
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).0051;
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tive; dermatological;
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Use of papillomavirus

E2 protein peptidomimetics

for treating

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      including growth of PV preneoplastic and neoplastic lesions, cutaneous lesions chosen from warts and other benign cutaneous lesions, plantar warts (verruca plantaris), common warts (verruca planta), Butcher's common warts, flat warts, genital warts (condyloma acuminatum) and epidermodysplasia verruciformis, laryngeal, oral, pharyngeal, oesophageal and other upper airway papilloma or vaginal, cervical, vulvar, penile and anorectal carcinoma. The EZ inhibitors may also be used to treat epithelial and internal fibropapillomas in animals. The present sequence represents a nucleotide sequence used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which competitively inhibits interaction of a papillomavirus (PV) E2 protein with a PV E1 protein for treating a cell infected with PV or mammal with a PV-induced condition. (A) has antiviral, virucide, cytostatic, antiproliferative and Annual antiviral, virucide,
                                                                                                                                                                               Co-activator domain; P300/CBP KIX domain; erythrocythaemia; skin disease; polycythaemia; haemoglobinopathy; cell differentiation; ulcer; cancer; neurological condition; neurodegenerative disease; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 912 BP; 149 A; 354 C; 287 G; 122 T; 0 other;
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                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                     HSV-1 VP22 coding
                                                                                                                                                                                                                                                                                                                                           05-NOV-2001
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method of identifying the co-activator domain of specific synthetic activators, involving contacting the target domain of a selected transcription factor with a peptide display library, and identifying those sequences which bind to the target domain. In particular, those which bind to the KIX domain of p300/CBP are useful. The peptides can be used in the treatment of diseases related to aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying co-activator domain specific transcriptional activators contacting a target domain of a selected transcription factor with epeptide display library, where the identified binding peptides are useful for reducing hyperglycemia -
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Best Local S
Matches 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a cdc4 phospho design (CPD) motif, (C), that targets molecules for ubiquitin dependent proteolysis. (C) have cytostatic, nootropic and antiproliferative activity. Also described is a method for the treatment of a disease or condition where affected cells have a defective protein, comprising administering (C) to promote degradation of the target protein in cells by ubiquitin dependent proteolysis. (C) can also be used for modulating the proliferation, growth and/or differentiation of cells. (C) can be used to modulate biquitin dependent proteolysis or cell proliferation, growth and or differentiation of cells. (C) is useful in the treatment of cancers and neurodegenerative disorders as well as spinal degeneration. The present sequence encodes the HSV-1 VP22 protein which is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Cdc4 Phospho Design motif that targets molecules for ubiquitin dependent proteolysis, is useful for the modulation of cell proliferation i.e. cancer treatment -
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 912 BP; 149 A; 354 C; 287 G; 122 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 30; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-164074/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nash P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2000; 2000US-202166P.
24-JAN-2001; 2001US-263774P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2001; 2001WO-CA00632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ubiquitin dependent proteolysis modulation; cdc4 phospho design motif; CDP motif; cytostatic; nootropic; antiproliferative; cell proliferation; growth; differentiation; cancer; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200183518-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                 183
                                                                                                                                                                                                                                                                     325
                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUNT SINAI HOSPITAL
                                          GGGTTCCTCCTCCGCGGTGCCCTCCCGAGACCCTTGCGACGGCCGTGGGGACCCCCGCCCCCC
                                                                                    CCAGAATCCGCCGCACTCCCAGACGCCCCCCGCGTCGACGGCGCCAACCCGATCCAAGACA
                                                                                                                               AACCGGACCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCA
                                                                                                                                                                            GCGACTAAGGCCCCCGCGGCCGCGGCGGCGGAGACCACCCGCGGCAGGAAATCGGCCCAG
                                                                                                                                                                                                                    ATGGCAAAGACCCCGTCGTTCGCGGTGGCGGCGGTCGCCGGAGGCCGGGCCGGTTCAC
    CCCGCGCAGGGGCTGGCCAGAAAGCTGCACTTTAGCACCGCCCCCCAAACCCCGACGCG
                                                                                                                                                                                                                                                              TCCGGAGGGCCGGACGCACACCACCACCACCGCCCCGGGCCCCCGGAACCCAGCGGGTG
                                                                                                                                                                                                                                                                                                         TCGGCTCGAGTTTGATCCGAGCCCACAGTCTCTCCTCGGGCCCACCGCGTCCGACCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pawson T,
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /partial
/product= "HSV-1 VP22 protein"
/transl_except= (pos:376..378,Gly)
/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds.
                                                                                                                                                                                                                                                                                                                                                      ٥,
                                                                                                                                                                                                                                                                                                                                                   Score 48.2; DB 24; Length Pred. No. 0.0051; o; Mismatches 163; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              912;
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Query Match
Best Local Simi
Matches 146;
                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes the herpes simplex virus (HSV) tegument protein VP22. VP22 was used in the preparation of a novernantiviral agent, which inhibits the maturation and/or replication of HSV by disrupting association between VP22 and VP16 and/or gB. The agent can be used to treat, e.g. cold sores, genital herpes, which can be used to treat, e.g. cold sores, genital herpes,
                                                                                                                                                                                                                                                                                                      Sequence 950 BP; 154 A; 365 C; 301 G; 130 T; 0 other;
                                                                                                                                                                                                                                                                                                                                             chickenpox and shingles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Pages 49-50; 75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antiviral agent disrupting binding of VP22 to VP16 or gB useful for treating infections caused by herpes simplex, e.g. sores and chicken-pox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-130696/12.
P-PSDB; AAW47194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV17085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV17085 standard; DNA; 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tegument protein; VP22; UL49; antiviral agent; treatment; sore; genital herpes; chickenpox; shingles; ds.
                       123
                                                             426
                                                                                                                                           366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
                                                                                                  63
                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   simplex virus
                                                                                                                                                                                                                                               Similarity
AACCGGACCCAGCTCCTCCTCCTCCTCCTCGTGGCCGCAGCCTCCGCATCCACAGCA
                                                             GCGACTAAGGCCCCCGGGCGCCGGCGGCGGAGACCACCCGCGGCAGGAAATCGGCCCAG
                                                                                         ATGGCAAAGACCCCGTCGTTCGCCGGTGGCGGCCGGTCGCCGGGCCGGGCCGGTTCAC
                                                                                                                                                                                TCGGCTCGAGTTTGATCCGAGCCCACAGTCTCTCCTCGGGCCCACCGCGTCCGACCGGCG
                                                                                                                                           TCCGGAGGGGCCGGACGCACCACCACCGCCCCCGGGCCCCCGAACCCAGCGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           creececc 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGTCTCC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATGGACCCCCGGGTGGCCGGCTTTAACAAGCGCGTCTTCTGCGCCGCGGTCGGGCGC 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTC
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96GB-0015726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
45..950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= VP22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       덛
                                                                                                                                                                                                                                         2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UL49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McLaughlan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
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                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                           Score 48.2;
Pred. No. 0
                                                                                                                                                                                                                          Mismatches 163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rixon
                                                                                                                                                                                                                                               . 0052 ;
                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                            of a novel
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AAH21
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Best Local S
Matches 146
                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a fusion protein comprising cell import and/or export signal sequences and an antigen which is suitable for immunizing an individual against a disease, together with a DNA that codes for said protein. The invention also relates to the use of the protein (II) and its encoding DNA (I) for immunizing an individual against diseases, in particular against infection-induced auto-immune and tumor disease. This sequence represents a DNA fragment which encodes the fusion construct vP22-E7 which is used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying an immunization agent comprising cell import and/or export signal sequences and an antigen for immunizing against infection-induced auto-immune and tumor disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein; VP22; E7; cell import signal; cell export signal; antigen; immunization; infection-induced auto-immune disease; tumor disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH21456 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200151516-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VP22/E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-2001
                                                                                                                                                                                                                                                                                                                                    Sequence 1225 BP; 246 A; 418 C; 358 G; 203 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 23pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-442135/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JAN-2000; 2000DE-1001230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-2001; 2001WO-DE00134.
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388
                                                                                                            328
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                                                                                                                                                                                                                                                          Similarity
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GCGACTAAGGCCCCCGGCCCCCGGCGGCGGAGACCACCCGCGCAGGAAATCGGCCCAG
                                                                                                                                                 TCGGCTCGAGTTTGATCCGAGCCCACAGTCTCTCCTCGGGCCCACCGCGTCCGACCGGCG
                                                    2.8%;
nilarity 47.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michel N,
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                                                                                                                                                                                                                                                    Score 48.2;
Pred. No. 0.
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                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                           163;
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                                                                                                                                                                                                                                                                                Length 1225;
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RESULT 15
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15-FEB-2001;
04-APR-2001;
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                                   WPI; 2002-257367/30
P-PSDB; AAU77235.
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                                                                                                                                                                                                                                                                                              2001US-281004P
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2001US-268575P
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The present invention relates to a new nucleic acid molecule that CC encodes a fusion polypeptide. The fusion protein comprises a first polypeptide comprising at least one intercellular transport polypeptide CC and a second polypeptide comprising at least one antigenic polypeptide CC are peptide. The invention also describes an optional linker peptide CC linking the first and second polypeptide. The nucleic acid is useful as CC a vaccine for enhancing immune responses, primarily cytotoxic T lymphocyte responses to specific antigens such as tumour or viral CC lymphocyte responses to specific antigens such as tumour or viral CC useful as a therappeutic vaccine for cancer and for major chronic viral CC infections, as well as in the treatment of veterinary herpesvirus infections, including equine or bovine herpesvirus, Marek's disease virus CC infections, including equine or bovine herpesvirus, Marek's disease virus CC infections. The present nucleic acid sequence encodes the pcDNA3-VP22/E7 creation of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.8%;
Best Local Similarity 47.2%;
Matches 146; Conservative (
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                                                                                                                                                                                                                                                                                                        442 CCAGAATCCGCCGCACTCCCAGACGCCCCCGCGTCGACGGCGCCAACCCGATCCAAGACA.501
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CCATGGACCCCCGGGTGGCCGGCTTTAACAAGCGCGTCTTCTGCGCCGCGGTCGGGCGC
                                                                   CTCAACACCGCCGTCGCCAGCGGGAGTCCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTC 302
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Match Length
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       .9 1926 4 US-09-249-585A-4
9 1931 2 US-09-130-1114-2
8 9191 4 US-09-247-504-11
8 950 4 US-09-230-421-1
1.8 950 4 US-09-230-421-1
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1.7 43.280 2 US-08-680-506-5
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1.7 1587 3 US-08-680-506-6
1.7 2233 3 US-08-680-506-6
1.7 233 3 US-08-680-506-2
1.7 4403765 4 US-09-103-840A-2
1.7 4411529 4 US-09-103-840A-2
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1.7 1905 4 US-09-103-840A-1
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1.7 1915 4 US-08-222-463-14
1.5 1221 1 US-08-241-766-10
1.5 1257 3 US-08-241-766-10
1.5 1257 4 US-08-241-766-10
1.5 1257 1 US-08-431-659-1
1.5 1257 1 US-08-433-659-1
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1.5 1258 1 US-08-433-659-1
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 Sequence 4, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 1, Appli
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RESULT 2
US-09-130-114-2
US-09-130-114-2
; Sequence 2, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: HOrlick, Robert A.
; APPLICANT: Damaj, Bassam B.
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| | US SERVICE | S B S . | 0 0 | α α | a |
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| Matches | CURRENT AP CURRENT FI NUMBER OF SOFTWARE: SEQ ID NO 4 LENGTH: ID TYPE: DNA ORGANISM: FEATURE: NAME/KEY: LOCATION: OTHER INF 109-249-585 Query Match Best Local | 7 E E 2 E E 2 L | 441 441 442 443 443 443 443 443 | 332 332 332 332 333 333 333 333 333 333 | ο ω ο |
| 97 TCG 97 TCG 157 CCC 157 CCC 217 CCC 531 TCC | im im | 9-585A-4 ice 4, Applicati ice 4, Applicati ice 6417002 iL INFORMATION: CANT: Horlick, OF INVENTION: | ww00000 | | 1.8 |
| CONBETVAL CCGGAGGCC CCCCCCCCCCCCCCCCCCCCCCCCCCC | LICATION WILLICATION WILLICATION WILLIAM TO MAKE THE ATTENT OF THE ATTEN | | 4 4 4 4 W W | ****** | |
| COMMENTATIVE | yir | ion US/0924 Robert Robert RETHOLFOR | 691777 | 1224000000 | 00004 |
| GCTC | st | · w | 1 US | 2 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | us us |
| GTCCT GTCCT GTCCCC GTCCCC GTCCCC GTCCCC GTCCCC GTCCCC GTCCCC GTCCCC GTCCCCC GTCCCCC GTCCCCC GTCCCCC GTCCCCC GTCCCCCC GTCCCCCCC GTCCCCCCC GTCCCCCCCC | 09/ 1 rai Pre | MA 58 | 8-08-1 | | -08- |
| PISMACO PICACAACO PICACAAC |),58 of E No. | ALIGNMENTS 5A | 09-722-00 | 08-474-93 | 94.5 |
| cones 1 | /A-1 DB | rs and | 73-1 73-1 21A-1 59-1 68A-11 01A-2 | 3-1 3-1 3-1 3-1 3-1 | 6A- 0-1 |
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| TCCTC | | EPISOMES | ושו שו שו שו שו שו | י עו | 10 10 |
| CGICC COTOCO CONOCO CON | | ũ | Api Api Api Api Api Api Api | 6, Appli 32, Appli 5, Appli 19, Appli 19, Appli 1, Appli 1, Appli 1, Appli 1, Appli | , App App |
| 156 470 216 530 576 | | | | ֧֧֧֧֧֧֧֧֧֧֧֧֚֚֚֚֚֓֞֟֟֞֟֟֟֓֓֟֟֓֟֓֓֟֟֟֟֟֝֟֝֟֝֟֝֓֓֟֝֟֝֟֝֟֝֟֝֝֟֝֟֝֝֟֝֝֟֝֟֝֝֟֝֝֟֝֟֝֝֟֝֜֝֟֝֜ | |

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FILE REFERENCE: 0867/LD903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SCO ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1931
TYPE: DNA
ORGANISM: EBNA
US-09-130-114-2
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                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Ndel-EcoR1 OTHER INFORMATION: fragment US-09-347-504-11
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Howley, Peter M.

APPLICANT: Benson, John

APPLICANT: Kasukawa, Hiroaki
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELL
FILE REFERENCE: HAV-041.01
CURRENT APPLICATION NUMBER: US/09/347,504
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
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US-09-347-504-11
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SEQ ID NO 11
LENGTH: 912
TYPE: DNA
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Best Local Similarity
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Best Local Similarity
Matches 117; Conserv
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TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                            123
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                                                                                              ATGGCAAAAGACCCCGTCGTTCGCGGTGGCGGCGGTCGCGGAGGCCGGGCCGGGTTCAC 122
                                                                                                                                                        TCGGCTCGAGTTTGATCCGAGCCCACAGTCTCTCTCGGGCCCACCGCGTCCGACCGGCG
                    AACCGGACCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCA 182
                                                                   GCGACTAAGGCCCCGGGGGGCGGCGGGGAGACCACCCGGGGAGGAAATCGGCCCAG
                                                                                                                             TCCGGAGGGGCCGGACGCACACCACCACCACCGCCCCGGGCCCCCGAACCCAGCGGGTG
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Pred. No. 0.001;
0; Mismatches 163;
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Pred. No. 0.0008;
0; Mismatches 113;
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                                                                                                                                                                                                                  Length 912;
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US-US-22.

Sequence 14, Application US-702.

Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F.
SAPPLICANT: FALKNER, F.
FITTLE OF INTENTION: RECOMBINANT FOWLPOX VIRUS

TITLE OF SEQUENCES: 52
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; TYPE: DNA
; ORGANISM: HERPESVIRUS
US-09-230-421-1
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US-09-230-421-1
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CURRENT APPLICATION NUMBER: US/09/230,421
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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Patent No. 6200577
GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P18189C
                                                                                                                                                                                                                                                           123 AACCGGACCCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCA 182
                                                                                                                                                                                                                                                                                                                                                                                                                             366 TCCGGAGGGGCCGGACGCACCACCACCACCACCACCAGGGCCCCCGAACCCAGCGGGTG
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Similarity 47.2%;
                                                                                                  CCCGCGCAGGGGCCCAGAAAGCTGCACTTTAGCACCGCCCCCCAAACCCCGACGCG 605
                                                                                                                                                                                                          CCAGAATCCGCCGCACTCCCAGACGCCCCCCGCGTCGACGGCGCCAACCCGATCCAAGACA
                                                                                                                                                                                                                                                                                                                     GCGACTAAGGCCCCCGCGGCGGCGGCGGCGGAGACCACCCGCGCAGGAAATCGGCCCAG
CCATGGACCCCCGGGTGGCCGGCTTTAACAAGCGCGTCTTCTGCGCCGCGGTCGGGCGC
                                              CTCAACACCGCCGTCGCCAGCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTC 302
                                                                                                                                                         CCATGGACCCCCGGGTGGCCGGCTTTAACAAGCGCGTCTTCTGCGCCGGGCGGTCGGGCGC 624
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Pred. No. 0.0011
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                                                                                                                                         RESULT 6
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Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 harm
                                                                                    Sequence 1, Application US/08804227C Patent No. 5876991
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APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                GENERAL INFORMATION:
APPLICANT: DeHoff
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IMMEDIATE SOURCE:
CLONE: pTZgpt-
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ZIP: 22313-0299
ZOPUTER READABLE FORM:
COMPUTER: FLOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: OCTOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
   APPLICANT:
                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                             275 CGGGTTCATGAGGTCCAAGCTCGTGCTCCTCGTCTCCCATGAGCTCTCCCCTCTCTGGTGG 334
                                                                                                                                                                                                                                                                                                                                                                 215 TTGCGACGGCCGTGGGGACCCCCGCCCCTCAACACCGCCGTCGCCAGCGGGAGTCCCCCT 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 2.8%; Score 47.4; DB 1; Length 7218; I Similarity 4.4%; Pred. No. 0.0049; 12; Conservative 160; Mismatches 101; Indels 0
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Kuhstoss, Stuart A. Rosteck, Paul R., Jr. Sutton, Kimberly L.
                                                  DeHoff, Bradley S.
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LOCATION:
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US-08-804-227C-1
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSES: THOWAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
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NAME/KEY:
LOCATION:
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REGISTRATION NUMBER: 35,784
REFERENCELDOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 43280 base pairs
TYPE: nucleic acid
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CGAAGGCAGGCTCGTCCT 18327
                                                                                                                                                                                              GGACCCCGCCCCTCAACACCCCCGTCGCCAGCGGGAGTCCCCTCGGGTTCATGAGGTC 289
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14351..19945
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US-08-680-506-5

Sequence 5, Application US/08680506C

Sequence 5, Application US/08680506C

Patent No. 6008013

GENERAL INFORMATION:
APPLICANT: REYNOLDS, PAUL R.

TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091

CURRENT APPLICATION NUMBER: US/08/680,506C

CURRENT FILING DATE: 1996-07-08

EARLIER APPLICATION NUMBER: 60/021,672

EARLIER FILING DATE: 1966-07-05

NUMBER: OF SEQ ID NOS: 18

SOPTMARE: Patentin Ver. 2.0

EEQ ID NO 5

LENGTH: 954

TYPE: DNA
                                                                                                                                                                                                                                                                  APPLICANT: REPORTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 8
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US-08-680-506-8
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Best Local S
Matches 97
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Best Local (
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TYPE: DNA
ORGANISM: Gallus gallus
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ORGANISM: Gallus gallus
                                                                                                                                                     Match 2.7%;
Local Similarity 53.6%;
                           139 TCCTCCTCCTCCTCGCGCCGCCGCCACCCCACAGGGGTTCCTCCTCCGCG 198
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97; Conserv
Conservative
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53.6%;
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                                                                                                                                    Score 46.6; DB 3; Length 1347;
Pred. No. 0.0035;
0; Mismatches 84; Indels 0
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CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 2233
TYPE: DNA
ORGANISM: Gallus gallus
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                                                                            US-08-680-506-4
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US-08-680-506-4
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TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 18
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US-08-680-506-6
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Query Match 2.7%; Score 46.6; DB 3; Length 2233; Best Local Similarity 53.6%; Pred. No. 0.0045; Matches 97; Conservative 0; Mismatches 84; Indels 0
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                                                                                                                                                                                                                                                                            APPLICANT: Reynolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/60091
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LENGTH: 1587
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Local Similarity 53.6%;
les 97; Conservative
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Gaps

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APPLICANT: Reymolds, Paul R.
TITLE OF INVENTION: CHONDROCYTE PROTEINS
FILE REFERENCE: 176/6091
CURRENT APPLICATION NUMBER: US/08/680,506C
CURRENT FILING DATE: 1996-07-08
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER APPLICATION NUMBER: 60/021,672
EARLIER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 5027
TYPE: DNA
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: THEERCULOSIS
FILE REFERENCES: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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US-08-680-506-2
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US-09-103-840A-2/c
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GENERAL INFORMATION:
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Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FIRSISCHMAN, Robert D.
APPLICANT: FYRASER, Claire
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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US-09-103-840A-2
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Best Local Similarity 52.9%;
Matches 99; Conservative
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SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 4403765
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Best Local :
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ORGANISM: Mycobacterium tuberculosis
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCCTTGCGACGGCCGTGGGGACCCCGCCGCCGTCAACACCGCCGTCGCCAGCGGGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ceeceercecceeaeecceerreacaacceeaeccaecrecrecrecrecrecrecrecrec 150
                                                                                                                                                                                                                                                                                                                                                              CCCTCGG 277
                                                                      CCGGTTCCTCCGGTGCCGGCCGCCCGCCGGCCCCGGCGTTACCGCCAGTC 3932413
                                                                                                                                                                                                                    GCGCCGCCTTGGCCGCCGGTGCCGGATACCGGCCTTGCCCGGCGGCGCCGACAACCCCCG 3932473
                                                                                                                                                                                                                                                                                   TCGTGGCCGTCGCAGCCTCCGCATCCACAGCAGGGTTCCTCCTCCGCGGTGCCCTGCGAG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCGGTCGCCGGAGGCCGGGCCGGTTCACAACCGGACCCAGCTCCTCCTCCTCCTCC 150
                                                                                                                                         ACCCTTGCGACGGCCGTGGGGACCCCGCCGCCGCCCTCAACACCGCCGTCGCCAGCGGGAGTC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46.2; DB 4; Length 4411529; Pred. No. 0.27; 0; Mismatches 88; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1905 base pairs
LENGTH: Nucleic acid
TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-142-623-2
                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09142623 Patent No. 6337201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Koji Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 98-0989*/LC(WMC)/144
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/1
FILING DATE: September 10,
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KOJI YANAI et al.
IITLE OF INVENTION: -FRUCTOF
IITLE OF INVENTION: ISOLATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: mat peptide LOCATION: 1 .. 1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2033 K S. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                      524
                                                                                    190 rccrccccccrcccaca 211
                                                                                                                        464 GCCCGTCATCGCCGACCACCCCTTCGCCGTCGACGTCACCGCCTTCCGCGATCCGTTTG 523
                                                                                                                                                                                                 404 AGACGCAGTCGTTGGCCGTCGCGCGCGGCGGCCGCCTCCGACAAGCTCGACCAGG
                                                                                                                                                           130 CCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCAGGTTCC 189
                                                                                                                                                                                                                                                                            82;
                                                                                                                                                                                                                                 70 AGACCCCGTCGTTCGCGGTGGCGGCGGTCGCCGGAGGCCGGGTCGACAACCGGA 129
                                                                                                                                                                                                                                                                        h 2.7%;
Similarity 57.7%;
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20006
                                                    TCTTCCCCAGTCCCAAGTTGGA 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Wenderoth, Lind & Ponack, L.L.P. 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Microorganism: Aspergillus niger ACE-2-1 (ATCC 20611)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF ISOLATING -FRUCTOFURANOSIDASE GENE, SYSTEM FOR FRUCTOFURANOSIDASE, AND -FRUCTOFURANOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09/142,623
ber 10, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.5 inch, 1.44
                                                                                                                                                                                                                                                                        Score 46; DB 4; Length 1905; Pred. No. 0.0061; 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM FOR PRODUCING NOSIDASE VARIANT
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                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                               463
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Sequence 2, Application US/09103840A

Patent No. 6294328

(GENERAL INFORMATION:
APPLICANT: HITE; Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WINTER, Claire M.
APPLICANT: VENTER, JOHn C.
ITITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
ITITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.6%;
Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                   674928 CCCGCCTCGGCCGCTTTTCCGCCGGCCCGCCGGCGCCATCCTGGCCGCGGCACC 674987
                                                                                                                                                                                                                                                    674868 GCCGCCGGCCTTGGCTGCCGGTTGTGCCCGCCGGCCCGGCCCGGCCCGGCCCGGC 674927
                                                                                                                                                                                                                                                                                                                                           674808 GCCGTTAGCGCCGTTGCCGCCGTCACCGGGGTCCCCGCCGCTGCCGCCGCTGCCGCTGCCGCTT 674867
                                                                                                             222 GGCCGTGGGGACCCCGCCGCCCTCAACACCCGCCGTCGCC 260
                                                                                                                                                                                                     162 GCAGCCTCCGCATCCACAGCAGGGTTCCTCCTCCGCGGTGCCCTGCGAGACCCTTGCGAC
                                                                                                                                                                                                                                                                                              102 GGAGGCCGCGGCCCGGTTCACAACCGGACCCCAGCTCCTCCTCCTCCTCCTCCTCGTGGCCGTC 161
                                                                                                                                                                                                                                                                                                                                                                                      42 GCCCACCGCGTCCGACCGGCGATGGCAAAGACCCCGTCGTTCGCGGTGGCGGCGGTCGCC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
4,
2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
  22:07:32
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44.6; DB 4; Length 4. Pred. No. 0.74; 0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4403765,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Search completed: July Job time: 89 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                         262
257
52.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          July 4, 2003, 21:37:15; Search time 211 Seconds (without alignments)
12591.504 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
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1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/ICT NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO5_NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
         6 10 US-09-923-876-6035

7 10 US-09-923-876-6078

7 9 US-10-128-714-5250

5 9 US-10-156-761-3022

6 9 US-10-156-761-31

2 8 US-08-902-572-13

2 9 US-10-161-499-11

2 10 US-09-682-179A-40

8 9 US-10-156-761-5655

8 9 US-10-186-761-1

2 10 US-09-682-179A-40

9 US-10-186-761-1

10 US-09-186-761-1

10 US-09-186-761-1

10 US-09-186-761-1

10 US-10-184-634-332

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Sequence 6035, Ap
Sequence 6078, Ap
Sequence 250, Ap
Sequence 3022, Ap
Sequence 1, Appli
Sequence 11, Appl
Sequence 14, Appl
Sequence 40, Appl
Sequence 40, Appli
Sequence 332, App
Sequence 332, App
Sequence 1894, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 375, Ap
Sequence 375, Ap
Sequence 375, Ap
Sequence 6250, Ap
Sequence 6250, Ap
Sequence 6250, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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US-09-923-876-6035
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | | 37 | 36 | | 34 | 33 | 32 | 31 | 30 | | | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
| 42 | 42 | 42 | 42 | 42 | 42 | 42 | 42.2 | 42.4 | 42.4 | 42.6 | 42.8 | 42.8 | 42.8 | 42.8 | 43 | 43 | 43.2 | 43.8 | 44.2 | 44.4 | 44.4 | 44.4 | 44.6 | 44.8 | 45 |
| 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.5 | 2.6 | 2.6 | 2.6 | 2.6 | 2.6 | 2.6 | 2.6 | 2.6 |
| 42999 | 42999 | 42999 | 42999 | 42999 | 42999 | 5025 | 4257 | 395 | 390 | 1428 | 3432 | 2790 | 2334 | 1440 | 1140 | 849 | 1143 | 41936 | 2855 | 2531 | 2480 | 2480 | 738 | 1662 | 978 |
| 9 | 9 | 9 | 9 | 9 | 9 | 10 | 9 | 10 | 10 | 9 | 9 | ø | 9 | 9 | 9 | 9 | 9 | 10 | 9 | 9 | 9 | 9 | 9 | 9 | 9 |
| US-10-219-694-17 | US-10-287-313-17 | US-10-151-081-17 | US-09-836-911A-17 | US-10-125-767-17 | US-09-799-462A-17 | US-09-960-253-176 | US-09-825-288A-1 | US-09-960-352-6638 | US-09-960-352-14023 | US-10-156-761-5428 | US-10-300-834-4 | US-10-300-834-5 | US-10-156-761-2734 | US-10-156-761-6190 | US-10-156-761-6044 | US-10-156-761-7075 | US-10-156-761-5707 | US-09-967-768A-116 | US-09-904-420A-1 | US-10-098-841-185 | US-10-098-841-186 | US-10-098-841-184 | US-10-156-761-276 | US-10-156-761-3483 | US-10-156-761-1779 |
| Sequence 17, Appl | Sequence 176, App | Sequence 1, Appli | Sequence 6638, Ap | Sequence 14023, A | Sequence 5428, Ap | Sequence 4, Appli | Sequence 5, Appli | Sequence 2734, Ap | Sequence 6190, Ap | Sequence 6044, Ap | Sequence 7075, Ap | Sequence 5707, Ap | Sequence 116, App | Sequence 1, Appli | Sequence 185, App | Sequence 186, App | Sequence 184, App | Sequence 276, App | Sequence 3483, Ap | Sequence 1779, Ap |

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL Program

SEQ ID NO 6035

LENGTH: 276

TYPE: DNA
ORGANISM: Zea mays
PEATURE:
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700458234H1
NAME/KEY: USCATION: 200, 275

OTHER INFORMATION: a, t, c, g, or other
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6035, Application US/09923876

Patent No. US20020013958A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kemigaki, Laura Y. (Ito)
APPLICANT: Kemigaki, Laura Y. (Ito)
APPLICANT: Kemigaki, Laura Y. (Ito)
APPLICANT: Convictorities and Polypeptides Derived From CORN SEEDLING
FILLE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/238,329
PRIOR APPLICATION NUMBER: 09/238,331
PRIOR APPLICATION NUMBER: 66/085,331
PRIOR APPLICATION DATE: 1998-05-05
PRIOR FILING DATE: 1998-05-05
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Best Local Similarity
Matches 273; Conserv
                                                                                                                                               1034 CARATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCA 1093
                                   1094 TTTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGTGCTTCTTCA 1153
61
                                                                                                               _
                                                                                                                   CAAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCA
TTTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCA 120
                                                                                                                                                                                                                         15.4%; Score 262; DB 10; Length 276; ilarity 99.3%; Pred. No. 1.1e-72; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                   1; Indels 1;
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S 밁 5 밁

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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEED
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-05-05
NUMBER OF 5EQ ID NOS: 6332
SOPTWARE: PERL PROGram
SEQ ID NO 6078
LENGTH: 257
TYPE: DNA
OPGANYSM. 750 mayor
                                                                                                                           RESULT 3
US-10-128-714-250
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US-09-923-876-6078
; Sequence 6078, Application US/09923876
; Patent No. US20220013958A1
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  Sequence 250, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 257; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700458322H1
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100.0%; Prr
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Pred. No. 4e-71;
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US-10-128-714-5250
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; SEQ ID NO 250
; LENGTH: 2997
; TYPE: DNA
; ORGANIZSM: Aspergillus fumigatus
US-10-128-714-250
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                                                                                                                                                                                                                                                                Sequence 5250, Application US/10128714 Publication No. US20030119013A1 GENERAL INFORMATION:
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Best Local Similarity 48.1%;
Matches 149; Conservative
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
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5 밁 S 밁 δ 밁 δ 밁 Ş

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APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
ITILE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
ITILE OF INVENTION: Methods of Use
ILLE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-09-09
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1173 GAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACG 1232
2463 GCAATGGGTGACAGGCTCGAGGAGGAGATCACCGATATGCTCAGCAAGGAAAGACGGCCG 2522
                                                                1413 CACATGGCTGAGAGGATCGCGGCGGTGTTGAAGGATGTCCTGAGGAAATCACAGGAGCAC 1472
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; PRIOR APPLICATION NUMBER: US 60/287,066; PRIOR FILING DATE: 2001-04-27; PRIOR APPLICATION NUMBER: US 60/295,890; PRIOR PILLING DATE: 2001-06-05; PRIOR PILLING DATE: 2001-07-09; PRIOR APPLICATION NUMBER: US 60/316,362; PRIOR FILING DATE: 2001-09-31; PRIOR FILING DATE: 2001-08-31; NUMBER OF SEQ ID NOS: 8603; SOFTWARE: Patentin version 3.1; SEQ ID NO 5250; LENGTH: 3495; TYPE: DNA ORGANISM: Aspergillus fumigatus US-10-128-714-5250
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                                                                                                                          NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3022, Application US/10156761 Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                         APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYCSHI
APPLICANT: SHIBA, TADAYCSHI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
LENGTH: 1326
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1326)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 3.1%;
Local Similarity 48.1%;
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Pred. No. 3.6e-05;
0; Mismatches 161;
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                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
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US-10-156-761-1/c
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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Best Local Similarity 52.7%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                     Matches 108;
                                                                                                                                                                                                                                                                                                                                       Query Match 2.9%;
Best Local Similarity 52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION UNMER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 9025608
TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                      3794466 ACGGGCGTCGGCGCCGCTCGGCGCGGGCCGGGGCGCTCGCCTACGCACTGCTCGGGGAGAA 3794407
3794286 CCGCGTCCTCACCGTCGGATTCGCC 3794262
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                                                                          CCTCCTCGGCTGTGTCCCCCACGTGGCCCGGGCCGCCCCACCGACCACCTCACCCG 3794287
                                                                                                                  CACAGCAGGGTTCCTCCTCCGCGGTGCCCTGCGAGACCCTTGCGACGGCCGTGGGGACCC 235
                                                                                                                                                         CGCCGGGCACCCATCACGGCGCCCTCCAGGTCGTCGCCGTCGTCGTCGCCGCGGC
                                                                                                                                                                                      GGTTCACAACCGGACCCAGCTCCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATC 175
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                              cecceccica cacceccerces
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Pred. No. 0.00012;
0; Mismatches 97;
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RESULT 7
US-08-902-572-13
; Sequence 13, Application US/08902572
parent No. US20020068706A1
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Best Local Similarity
Matches 146; Conserv
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,572
FILING DATE: 29-JUL-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 912 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matchew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-069.03
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Beach, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: INHIBITORS OF CELL-CYCLE PROGRESSION RELATED THERETO
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  625
                                                                                                                                                  505 CCCGCGCAGGGGCTGGCCAGAAAGCTGCACTTTAGCACCGCCCCCCCAAACCCCGACGCG
                                                                                                                                                                                           183
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                                 CTCGTCTCC 311
CTGGCGGCC 633
                                                                      CCATGGACCCCCGGGTGGCCGGCTTTAACAAGCGCGTCTTCTGCGCCGCGGTCGGGCGC
                                                                                                          TCCGGAGGGGCCGACGCACCACCACCACCACCACCACCCCCGGGCCCCCGAACCCAGCGGGTG
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47.2%;
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Pred. No. 0.0003;
0; Mismatches 163; Indels
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APPLICANT: Lin, Danny
APPLICANT: Lin, Danny
APPLICANT: Pawson, Anthony
ITITE OF INVENTION: PEPTIDES THAT MODULATE TH
ITITE OF INVENTION: AND PDZ DOMAINS
FILE REFERENCE: MTSI-P01-009
CURRENT APPLICATION NUMBER: US/09/862,179A
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
LENGTH: 912
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KABUKAWA, HIROAKI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: DAPILLOMAVURUS-INFECTED CEI
FILE REFERENCE: HAV-041.01.
CURRENT APPLICATION NUMBER: US/10/161,499
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/347,504
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 912
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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publication No. US20030044427A
GENERAL INFORMATION:
APPLICANT: Howley, Peter M.
APPLICANT: Benson, John
APPLICANT: Kasukawa, Hiroaki
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US-10-161-499-11
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Patent No. US20020147306A1
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity
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47.2%;
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APPLICANT: ONUMAL, SATOSHI
APPLICANT: INSHAMA, JUN
APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, JUN
APPLICANT: ISHIKAMA, JUN
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-27697
PRIOR FILING DATE: 2001-08-02
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US-09-862-179A-40
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US-10-156-761-5655
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                                                                                                                                                                  Query Match
Best Local S
Matches 120
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SEQ ID NO 5655
LENGTH: 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.8%; Score 48.2; DB 10; Length Best Local Similarity 47.2%; Pred. No. 0.0003; Matches 146; Conservative 0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (1)..(918)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    445 CCAGAATCCGCCGCACTCCCAGACGCCCCCGCGTCGACGGCGCCAACCCGATCCAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 TCCGGAGGGGCCGGACGCACCCACCGCCCCCGGGCCCCCGGAACCCAGCGGGTG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                505 CCCGCGCAGGGCTGGCCAGAAAGCTGCACTTTAGCACCGCCCCCCAAACCCCGACGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AACCGGACCCAGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 GCGACTAAGGCCCCCGGCGCCCCGGCGGCGAGACCCCGCGGCAGGAAATCGGCCCAG 444
133
                                                                                                                                                                    120;
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                                                                                                                                                                                         Similarity
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                           AGCTCCTCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCAGGGTTCCTCC
                                                                                                                      CCCCGTCGTTCGCCGGTCGCCGCGCCGCGGAGGCCCGGGCCGGTTCACAACCGGACCC 132
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                                                                                   CCGGGTCCCGCGACCCGGAGTCGGCCGTCGACACCCCGCCGTATCGCCCAGCTCCTCGCCG
                                                                                                                                                                  2.8%;
ilarity 50.0%;
Conservative
                                                                                                                                                                    0
                                                                                                                                                                Score 48; DB 9; Length 918; Pred. No. 0.00034; 0; Mismatches 120; Indels
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APPLICANT: OMURA, SATOSHI
APPLICANT: ISEDA, HARUO
APPLICANT: ISEIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SKIRKI, YOSHIYUKI
APPLICANT: HATTORI, MOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-08-9
PRIOR FILING DATE: 2001-18-02
PRIOR FILING DATE: 100-18-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; PEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
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US-10-156-761-1
RESULT 12
US-10-184-644-332/c
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Publication No. US20030119018A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                             6860939 CCGGGTCCCGCGACCCGGAGTCGGCCGTCGACACCCCGCCGTATCGCCCAGCTCCTCGCCG 6860998
                                                                                                          6861119 CCGCCCCGGGCCTTCGCCACGGCGTGCGCCGAGGCCGCGCCCTGGATCGCCGCCGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 2.8%; Score 48; DB 9; Length 9025608; Similarity 50.0%; Pred. No. 0.3; 20; Conservative 0; Mismatches 120; Indels 0;
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                                                                                                                                                            CCGTCGCCAGCGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTCCTCGTCTCCC 312
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Sequence 332, Application US/10184644
Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddwki, Paul J.
APPLICANT: Godowki, Paul J.

APPLICANT:

Goddard, Audrey Godowski, Paul J. Gurney, Austin L.

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US-10-184-634-332/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT ETLING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 332
LENGTH: 520
                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Best Local
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 2.8%; Score 47; DB 9; Local Similarity 18.6%; Pred. No. 0.00047
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T: Zhang, Zemin
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
INVENTION: ACIDS ENCODING THE SAME
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                                                               Smith, Victoria Watanabe, Colin K. Wood, William I.
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                                                                                                                                  Gurney, Austin L.
Pan ...
                                                                                                                            Pan,James
                                                                                                                                                                                 Goddard, Audrey
                                                                                                                                                                                                       Desnoyers, Luc
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Smith, Victoria
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RESULT 14 US-10-156-761-1894

Sequence 1894, Application US/10156761 Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OMURA, SJ
APPLICANT: IEDDA, II
APPLICANT: ISHIKAWJ
APPLICANT: HORIKAWJ
APPLICANT: HORIKAWJ

ISHIKAWA, JUN HORIKAWA, HIROSHI SHIBA, TADAYOSHI

SATOSHI , HARUO

APPLICANT:

APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR TILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02

ORGANISM: Streptomyces avermitilis

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CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 332
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Best Local
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 520
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59
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CTA....R.BB 49
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                                ATAGGATGTTG 458
                                                                   .T..B..YSTC.T.D.C.
                                                                                                       TGGTGTGGATAACAAACCAGAGATCACAAGAAACAAATGATGTCACATATAGCTTGGAGC 447
                                                                                                                                              TCM.T..C..C.TC.KCKTCMDC..C.TC..CM.Y.KC.N.A.NHBY...D.DSBYBWA. 120
                                                                                                                                                                                CTGGTGGTCCACTTTTACTGATGGAATTAGCATTTCTTCTGAGGCATGTTGGCTCGCAAG
                                                                                                                                                                                                                                                        GTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTCCTCGTCTCCATGAGCTCTCCCTCT 327
                                                                                                                                                                                                                                                                                            HCMTC..CT.C..C.YC.HCMSC.TC..CKBCTHCMKCYHCMSC..C.HCM.CMACA.CM
                                                                                                                                                                                                                                                                                                                                 GAGACCCTTGCGACGGCCGTGGGGACCCCCGCCGCCCTCAACACCCCCGTCGCCAGCGGGA 267
                                                                                                                                                                                                                                                                                                                                                                                                        TCCTCGTGGCCGCAGCCTCCGCATCCACAGCAGGGTTCCTCCTCCGCGGTGCCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCGGCGGTCGCCGGAGGCCGGGCCGGGTTCACAACCGGACCCAGCTCCTCCTCCTCC 147
                                                                                                                                                                                                                     .C.. CCHCMSCM.C..C.ACATC.MC.TC..CT.CMBC..C..CS.CATCHYCKTCM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                             .CY.CM.CMBC..CSSCMBC.HCM.CT.C.TCM.CT.C.SC..CMBCT.C.BCS.CMYC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%; Score 47; DB 9; Length 520
18.6%; Pred. No. 0.00047;
ative 89; Mismatches 262; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See File Wrapper or Palm
                                                                       .DTS..
                                                                     S.S.SH.TT.AHN..RK..BY.YT..N.B.BB..CT
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RESULT 15
US-09-990-385-2
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; NAME/KEY: CDS
; LOCATION: (1)..(1038)
US-10-156-761-1894
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Publication No. US20020192771A1

GENERAL INFORMATION:
APPLICANT: Koji YANAI et al.
TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE AND ITS GENE, METHOD OF
ISOLATING BETA-FRUCTOFURANOSIDASE GENE, SYSTEM FOR PRODUCI
BETA-FRUCTOFURANOSIDASE, AND BETA-FRUCTOFURANOSIDASE VARIA
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.7
Best Local Similarity 50.2
Matches 114; Conservative
                                                                                                                                                                                                                                      TELEFAX: 202-721-8250 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM COMPACIBLE
COMPUTER: IBM COMPACIBLE
COPENATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/09/990,385
FILING DATE: 10-Sep-198
PRIOR APPLICATION NUMBER: 09/142,623
APPLICATION NUMBER: 09/142,623
FILING DATE: September 10, 1998
ATTORNEY/ACENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 2001-1611
TELEBOONE: 2002-71,8200
                                                                                            TOPOLOGY: Linear MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488 CGCTGATCCTGCGCGACCTCGACCTCCTCGAGCAGGCCGCCGAGGTCACCGACGTCGGCA 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      548 TCTCCGTGTCCGTCGGCTTCACCGACCACGAGCTGTGGCGCACCGTC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 GCGGGAGTCCCCTCGGGTTCATGAGGTCCAAGCTCGTGCTCCTCGTC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 CCCTGCGAGACCCTTGCGACGGCCGTGGGGACCCCGCCGCCGCCTCAACACCGCCGTCGCCA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428 CCGGCATCATCGCGGCCCTGCGCGACCACGCGAACCCCTTCTCGATCCTCACCAAGGGCA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 TCCTCCTCCTCGTGGCCGTCGCAGCCTCCGCATCCACAGCAGGGTTCCTCCTCCGCGGTG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 TCGCGATGGGCACCAATGTCGACTGCTACCAGCGGGCCGAGGGCCGCTACCAGCTCATGC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 TCGCGGTGGCGGCGGTCGCCGGAGGCCGCGGGCCGGTTCACAACCGGACCCAGCTCCTCC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                              LENGTH: 1905 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.7%;
                                                   Microorganism: (ATCC 20611)
  mat peptide
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                                                                       Aspergillus niger ACE-2-1
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; LOCATION: 1 .. 1905; i IDENTIFICATION METHOD: E; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-990-385-2
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Search completed: July 4, 2003, 23:11:38 Job time: 236 secs
                                                                                    В
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                                                                                                                            190
                                                                                                                                                                                                        404 AGACGCAGTCGTTGGCCGTCGCGCGCGACGGCCGCCGCCGCTTCGACAAGCTCGACCAGG 463
                                                                                    524 TCTTCCGCAGTGCCAAGTTGGA 545
                                                                                                                                                                    464 GCCCCGTCATCGCCGACCACCCCTTCGCCGTCGACGTCACCGCCTTCCGCGATCCGTTTG 523
                                                                                                                                                                                                                                                                               70 AGACCCCGTCGTTCGCGGTGGCGGGCGGTCGCCGGAGGCCGGGCCGGGTCCACAACCGGA 129
                                                                                                                          rccrccccccrcccrcccaca 211
                                                                                                                                                                                                                                                                                                                                   0
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                               EST:*
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Gapop 10.0 , Gapext 1.0
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1702
1 attoggotogagtttgätoc.....gaggagatttoaatottagt 1702
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Copyright (c) 1993 - 2003 Compugen Ltd.
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em gss pro: *
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                                                                                                                                         RESULT 1
AY107383
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 512 | 519.6 | 551 | 612 | 615 | | Score |
| 30.1 | 30.5 | 32.4 | 36.0 | 36.1 | | % Query Match Length DB |
| 670 | 721 | .678 | 633 | | 843 | Length I |
| 14 | | | _ | 11 | 11 | ; <u> </u> |
| BQ788642 | BF629089 | BG464581 | AW067129 | AY108664 | AY107383 | DB ID |
| BQ788642 WHE4152_B | BF629089 HVSMEb000 | BG464581 EM1_71_E0 | AW067129 683016A01 | AY108664 Zea mays | | Description |

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|----------------|--------------------|----------------|----------------|----------------|--------------|-------------|-------------|--------------------|----------|----------|----------|----------|-------|----------|-------|---------------|-------|-------|-------|-------|-------------|------------------|------------------|---------------|---------|---------------|---------------|------------------|-------|--------|-------|------------------|-----------|------------------|----------------|-----------|-----------------|------------|
| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ა 5 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | œ | 7 |
| 101.6 | 101.6 | 102.2 | 104.6 | 125.4 | 125.8 | 129.6 | 131.6 | 134.2 | 135.8 | 148.6 | 150.2 | 154 | 158.2 | 160.4 | 171.2 | 185 | 185 | 186.2 | 202.6 | 203.2 | 203.2 | 211.2 | 215.8 | 218.4 | 302.8 | 307 | 314.4 | 314.4 | 325.4 | 327.2 | 342.4 | 360.4 | 375.2 | ω | 401.6 | 41 | | ò |
| | | | | | | | | | | ٠ | | | | | 0 | 10.9 | 0 | | | | :- | | | | 7. | 8 | œ | ω. | 9. | 9 | | - | .2 | ω · | ω. | 4 | ω. | 9 |
| 714 | 707 | 688 | 569 | 435 | 288 | 629 | 669 | 724 | 276 | 647 | 251 | 634 | 553 | 715 | 863 | 360 | 360 | 425 | 782 | 711 | 563 | 396 | 390 | 461 | 443 | 543 | 513 | 513 | 551 | 437 | 375 | 643 | 641 | 685 | 439 | 627 | 497 | 557 |
| 14 | 14 | 14 | Ľ | 14 | | | | | | 12 | 13 | 13 | 10 | 17 | 17 | 9 | 9 | 14 | 13 | 10 | 12 | 13 | 10 | 10 | 14 | 14 | 14 | 10 | 13 | 14 | 10 | 10 | 13 | 14 | 12 | 13 | 12 | 12 |
| Q11835 | BQ118269 | Q11474 | 126779 | Q66296 | 19 | w | Ü | | 02 | BF642258 | 2181 | 7334 | 7204 | | H5012 | AJ473498 | 47349 | 764 | 97127 | 65C | 7089 | 0827 | N | 0994 | 72 | 9625 | 840 | 0265 | 2163 | 6458 | 5786 | 674 | 7136 | 4837 | G56 | 990 | G26827 | 42 |
| 18358 EST60393 | BQ118269 EST603845 | 14748 EST60032 | 67795 NF111D09 | 62962 HS04P17u | 10193 SALK_C | 39738 AU239 | 171310 BJ17 | B21743 T31I17-T7 T | 026 AV54 | 258 NFC | 818 F047 | 349 BJ17 | 046 | 2 T31117 | 24 | 3498 AJ473498 | 3497 | _ | 7127 | 5650 | F270892 GA_ | J208273 BJ208273 | E022039 sm65g06. | E209946 so36h | 74729 C | Q296254 san89 | 8401 BRY_4306 | E402653 CSB010B1 | 630 | 464581 | 867 | W186747 BNLGHil3 | 361 NF050 | Q148371 NF067F07 | 60599 RHIZ2_59 | 09 HVSMEr | G268271 1000172 | 7 EM1_71_E |

ALIGNMENTS

| | | | /db_xref="taxon:4577" /clone="PC0096987" | | |
|-----------------|--------------|----------|--|-----------|------------|
| | | - | /db_xref="MaizeDB:635540" | | |
| | | | /organism="Zea mays" | | |
| | | | 1843 | | source |
| | | | Location/Qualifiers | | FEATURES |
| | | | Missouri, Columbia, MO 65211, USA | Misso | |
| ersity of | oject, Univ | ping Pro | Submitted (25-APR-2002) Maize Mapping Project, University of | Submi | JOURNAL |
| | | | Direct Submission | Direc | TITLE |
| | | | .C. | Coe, E.C. | AUTHORS |
| | | | (bases 1 to 843) | 2 (1 | REFERENCE |
| | | | Unpublished (2002) | Unput | JOURNAL |
| | | | Overgo Probes | Overg | |
| r Design of | equences fo | ensus Se | Maize Mapping Project/DuPont Consensus Sequences for Design of | Maize | TITLE |
| | Tingey, S. V | ,M. and | Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. | Arthu | |
| itt, M.S., | J.M., Whits | Voge1, | Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., | Haine | AUTHORS |
| | | , | (bases 1 to 843) | 1 (1 | REFERENCE |
| | | ; Zea. | clade; Panicoideae; Andropogoneae; Zea. | clade | |
| oaceae; PACC | Poales; F | iopsida | atophyta; Magnoliophyta; Lil | Spern | |
| ; Tracheophyta; | mbryophyta | phyta; I | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | Eukar | |
| • | | | ays | Zea mays | ORGANISM |
| | | | ays. | Zea mays. | SOURCE |
| | | | | HTC. | KEYWORDS |
| | | | AY107383.1 GI:21210461 | AY107 | VERSION |
| | | | 383 | AY107383 | ACCESSION |
| | | | ays PCO096987 mRNA sequence. | Zea mays | DEFINITION |
| HTC 25-MAY-2002 | linear | mRNA | 383 843 bp | AY107383 | LOCUS |
| | | | | | AYIO/383 |

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BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 827;
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Best Local Similarity
                                                                                                                                      670
                                                                                                                                                                                                                                                                                                                          490
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             790
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                              TGGAAGTTGCTGAAGACAAT-GTCGCAAGAAGAGTCCTACGGGAACATATTCGT
                                                                                             GCCTGAAAATACAGATGCCACAAACTTATGTTGTTCACCTGGGGAATAGTAAAGAACTAA
                                                                                                                                                     CTGGAGCCATGATTGATTCTCATACAACGGCTGAGTATTGGAATAGCAGGACTAGCGATC
                                                                                                                                                                                                                  TCCATGAAATGCGTGGGCATTACTTTAAGGTTGAATATGTCAAACATCTTCCCTTTGTTG
                                                                                                                                                                                                                                                           GGCTTGACCCTGTTCTGAAAGATCATGTTCCTAAAGTCCTTCCGAAGATTTTTGTGGTGGA
                                                                                                                                                                                                                                                                                                                                           CAGTTGATATTGCTCTAAAAGCTGATCTGGTTATCTTAAACACTGCTGTTGCTGGCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                        GCTTGGAGCATAGGATGTTGAACCATGGAGTGCAGGTTTTACCAGCTAGAGGACAGGAGG
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                                                                       GCCTGAAAATACAGATGCCACAAACTTATGTTGTTCACCTGGGGAATAGTAANGANCTAA
                                                                                                                                      CTGGAGCCATGATTGATT
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 615)
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Mapping Project Test of the Mapping Pro
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/db_xref="MaizeDB:635539"
/db_xref="taxon:4577"
/clone="PC0096986"
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|--|-----------------------------|--|-------------------------------|
| /note="Organ: EmbryopBluescript II from | | AGCAATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGAATCGT | 로 & |
| /db_xref="taxon:455: /clone_lib="Embryo" | | 573 TGATGTTGTTTCAGAATTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGA 514 | οь |
| | realureS source | 1139 TGATGTGCTTGTTCAGAATTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGA 1198 | Q |
| High quality sequence start: High quality sequence stop: POLYA=NO. | | 1079 TCATGACCGTGTCCATTTTGTGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAAT 1138 | Qy da |
| Sequences have been trimmed below Phred quality 16. The is 20. Seq primer: PolyTMix | | Query Match 36.0%; Score 612; DB 10; Length 633; Best Local Similarity 99.2%; Pred. No. 2.2e-147; Matches 612; Conservative 0; Mismatches 5; Indels 0; Gaps 0; | Query M Best Lo Matches |
| The University of Georgia, D. Plant Sciences Building, Rm. Tel: 706 542 1860 Fax: 706 583 0210 Fax: 706 583 0210 | | cioned, Stratag 161 a 174 | BASE COUNT ORIGIN |
| I database from Sorghi blished (2000) act: Cordonnier-Pratt I catory for Genomics and | TITLE JOURNAL COMMENT | <pre>/dev stage="14 days after pollination" /lab_host="DH10B" /note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap /note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap Express); Site_1: XhoI; Site_2: EcoRI; Directionally</pre> | |
| <pre>1 (bases 1 to 678) Reid, S.P., Cordonnier-Pratt,</pre> | REFERENCE AUTHORS | ı | |
| Euka Sper clad | | /cultivar="B03" /cultivar="B03" /db_xref="taxon:4577" /clone lib="683 - 14 day immature embryo from Hake lab (HS | |
| sorghum. | SOURCE | rce | nos |
| BG464581 BG464581.1 GI:13393230 | ACCESSION VERSION | | E E ATTITUDE C |
| BG464581 EM1_71_E08.g1_A002 Embryo 1 sequence. | DEFINITION | 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 | |
| | RESULT 4 BG464581 | ces | |
| | | AL Unpublished (1999) Contact: Walbot V | JOURNAL COMMENT |
| GATTGAGGAGATTTCAA | 40 A0 | | TITLE |
| CATTGAG | _ | | REFERENCE |
| .619 CCATGTCCGATTCTATTCCAATTCAT. | D Qy 1 | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade: Panicojdeae: Madronocomeae: 7ed | |
| 153 GTAAACTGTAGATTGCACTCTGTTGG | Db | _ | SOURCE ORGANISM |
| .559 GTAAACTGTAGATTGCACTCTGTTGG | | AW067129 AW067129.1 | ACCESSION VERSION |
| .499 ATCAGCTTGCGCTAACATGTTGAACT) | Qу 1 Db | AW067129 633 bp mRNA linear EST 12-OCT-1999 GB3016A01.x1 683 - 14 day immature embryo from Hake lab (HS) Zea mays cDNA, mRNA sequence. | LOCUS DEFINITION |
| 273 GTTGAAGGATGTCCTGAGGAAATCAC | | r 3 | RESULT 3 |
| 439 GTTGAAGGATGTCCTGAGGAAATCAC | Qy 1 | 601 AGAACATCGTCAGAC 615 | Db |
| 333 CTATGGCAGGGTGAAGGAAATGTTCA | da Vy | 1321 AGAACATCGTCAGAC 1335 | Qy |
| }= | | 1261 TGAACGGCTCGACTGGCCTTCTGCATCCTGCTGGAAGAGGGCGTGGGGCCTCTTGCAA 1320 | B & |
| 319 AAAGAACATCGTCAGACTCGCAAGCC | 0у 1 | CAATGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCC | ם פ |
| 8= | | CAATGGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCC | . Q |
| 1259 CCTGGACGGCTCGACTGGCCTTCTGC | | 421 ATGTGCTTGTTCAGAATTCTCAGGGCCGTGGAGAATGCTTTTGGAAGGATAACAATTGAAG 480 | Db |

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m bicolor"
558"
0 1 (EM1)"
0 1 (EM1)"
1 ryos germinated for 24 hr; Vector:
1 com Lambda Zap II; Site_1: XhoI; Site_2:
2 y was made from poly-A RNA in the cloning
                                                                                                                                                                       : 669
                                                                                                                                                                                                                                                                                                                                  1 Bioinformatics
Department of Plant Biology
n. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptophyta; Embryophyta; Tracheophyta;
.a; Liliopsida; Poales; Poaceae; PACC
>goneae; Sorghum.
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L (EM1) Sorghum bicolor cDNA, mRNA
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JOURNAL
COMMENT
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VERSION
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                                        Hordeum vulgare.
Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
Triticeae; Hordeum.
1 (bases I to 721)
Ving,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex drought-stressed seedling shoot cDNA
                                                                                                                                                                                                                                                    BF629089 721 bp mRNA
HVSMED0009N03f Hordeum vulgare seedling
HVCNMA0002 (Dehydration strees) Hordeum
HVSMED0009N03f, mRNA sequence.
Unpublished (2001)
On Dec 19, 2000 this sequence version
                                                                                                                                                                                                                           BF629089.2
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vulgare cDNA clone
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Email: rwing@clemson.edu
Total hq bases = 588
Seq primer: AATTAACCCTCACTAAAGGG
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Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
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                                                  TTAATGCTCAGACCAAATTTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTC 1080
                                                                                                                                                                                     TCATCCAACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAGTTGTGGGGAAGTGATG 1020
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TGAATGCTCAGACAAAGTTTGAGACACAGTTACGTGAATTTGTGGCGAAGAATGGGATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.genome.clemson.edu/projects/barley. To orde
this clone see http://www.genome.clemson.edu/orders Al
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gpages/bgn/31/cover.html)"
151 c 203 g 172 t
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/lab_host="TJC121"
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HVcDNA0002 (Dehydration stress)"
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/db_xref="taxon:4513"
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                                                                                                                                                                                                                                                                                                                                       genomes - Chinese Spring whole plant cDNA library Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ788642 670 bp mRNA linear WHE4152_B09_C18ZS Wheat CS whole plant cDNA library aestivum cDNA clone WHE4152_B09_C18, mRNA sequence.
BQ788642
                                                                                                                                                                                                                                                  Email: oandersn@pw.udda.gov
Sequences have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson,O.D., Akhunov,E., Chao,S., Crossman,C., De, Lazo,G.R., Rausch,C.J., Wilson,C. and Woo,J. The structure and function of the expressed portion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 670)
/cultivar="Chinese Spring"
/db xref="taxon:4565"
/clone="wHE4152_B09_C18"
/clone=lib="wHeat CS whole plant cDNA library"
/clone=lib="wHeat CS whole plant cDNA library"
/clone=lib="Wheat CS whole plant cDNA library"
/tissue_type="Roots, leaves, crown, stem and sheath"
/dev_stage="Adult"
/lab_host="Vector: Lambda Uni-ZAP XR, excised phagemid
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plant
tissues from wheat cv. CS grown to full tillering stage in
greenhouse were collected at University of California,
Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total
                                                                                                                                                                                                                                     Location/Qualifiers
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Query Match
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Matches 569; Conserv
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GI:13392578

Embryo

557 (EM1)

mRNA linear Sorghum bicolor

cDNA,

20-MAR-2001

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KEYWORDS
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1 (bases 1 to 557)

Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
ALEST database from Sorghum: developing embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 706 542 1860
Fax: 706 583 0210
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                                                                                          GAGATCAGAAGAAACAAATGATGTCACATATAGCTTGGAGCATAGGATGTTGAGCCATGG
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                            AGTGCAGGTTTTACCAGCTAGGGGACAGGAGGCAGTTGATATTGCTCTAAAAGCTGATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sorghum bicolor"
/db_xref="texon:4558"
/clone_lib="Embryo 1 (EM1)"
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Matches 494;
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Best Local Similarity
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                                                                    317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA, mRNA sequence.
BG268271
BG268271.1 GI:129730
EST.
Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: walbot@stanford.edu
Plate: 1000172 row: A colu
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGZ68271 497 bp mRNA linear EST 20-FEB-20
1000172A07.x2 1000 - Unigene I from Maize Genome Project Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize ESTs from various cDNA libraries sequenced at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
AAAGGGCTATGGCAGGGTGAAGGAAATGTTCATGGAGCACCACATGGCTGAGAGGATCGC 1432
                                                                                                                                                                                          GATCGTCCTGGACGGCTCGACTGGCCTTCTGCATCCTGCTGGGAAGGAGGGCGTGGCGCC 1312
                                                                                                                                                                                                                                                                               AATTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGA 1252
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                                                                                                    TCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGGTCTCCATGGGGGA 1372
                                                                                                                                                                                                                                                       AATTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGA
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                                                                       TCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGTCTCCATGGGGGA
                                                                                                                                                                 GATCGTCCTGGACGGCTCGACTGGCCTTCTGCATCCTGCGGAAGGAGGGCGTGGCGCC 318
                                                                                                                                                                                                                                                                                                                                               AGCAATTGATGTGCTTGTTCAGAATTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAAC
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650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="dbEST:687063C09.y1"
/db_xref="caxon:4577"
/db xref="caxon:4577"
/clone lib="1000 - Unigene I from Maize Genome Project"
/clone lib="1000 - Unigene I from Maize Genome Project"
/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660, 683
, 687, 707, and 945. Contigs were assembled using TiCR's
CAP program and a representative EST from each contig was
selected for the Unigene set. All singlets were also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Zea mays"
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Pred. No. 2e
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2e-116;
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BI959909
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 AAAGGGCTATGGCAGGGTGAAGGAAATGTTCATGGAGCACCACATGGCTGAGAGGATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          627 bp mRNA linear EST 22-OCT-2001
HVSMEn0022F11f Hordeum vulgare rachis EST library HVcDNA0015
(normal) Hordeum vulgare cDNA clone HVSMEn0022F11f, mRNA sequence.
B1959909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Tex: 864 656 4293
Tex: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticeae; Hordeum.

1 (bases 1 to 627)

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Frisch,D., Akkins,M., Yu,Y., Henry,D., Palmer,M., Ran,J., Oates,R. and Main,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI959909.1 GI:16311164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total hq bases = 508
Seq primer: AATTAACCCTCACTAAAGGG
Seq praintry sequence stop: 612.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGCCCATCAGCTTGCGCTAACATGTTGAACTAGATTTTACGGGCTACGCCTACGTGGTT
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/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: /Note 2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) CDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rwing@clemson.edu
                                                                                                                                                                                                                                                                                                    /tissue_type="Rachis"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                 clone_lib="Hordeum vulgare rachis EST library HVcDNA0015"
                                                                                                                                                                                                                                                                                                                                                                                                      organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                    lone="HVSMEn0022F11f"
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                           REFERENCE
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Best Local Similarity
Matches 479; Conserv
                                                                                                                                                                        sequence.
BG560599
BG560599.1
EST.
                                                                                                                                                                                                                                                        BG560599
RHIZ2_59_
  Sorghum propinquum.
Sorghum propinquum.
Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
(bases 1 to 439)
Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Prati, L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162
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                                                                                                                                                                                                                                                        439 bp mRNA linear EST 10-APR-2001
_D08.b1_A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
                                                                                                                                                                                               GI:13589597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 417; DB Pred. No. 6.2e 0; Mismatches
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contains a minimum of 100 bases of phred value above. For more details on library preparation
                            20
                            or
P
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sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgm/31/cover.html)"
a 135 c 185 g 143 t 2 others
                      DB 13;
.2e-97;
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| 1427 GATCGCGGCGGTGTTGAAGGATGTCCT | 1367 GGGGAAAAGGGCTATGGCAG | 1307 GGCGCCTCTTGCAAAGAACAT 438 CACGCCTCTCGCCAGGAACAT | 1247 CACGGAGATCGTCCTGGACGG | 1187 GATAACAATTGAAGCAATGGC 318 GATAACGATTGAAGCAATGGC | 1127 CTTGGCAGCAATTGATGTGCT | 1067 GAAGAACACGATTCATGACCG | 1007 TGTGGGAAGTGATGTTAATGC | 947 TCAGGCTTTGCAGCTCATCCA - 78 TCAGAGTCTGCAACTCATCCA | 888 GCAATAATAAACAGTGTATCA |
|--------------------------------------|---|---|---|--|---|---|---|--|--|
| TCT 1453 TTCT 584 | GGGGSAAAAGGGCTATGGCAGGGTGAAGGAAATGTTCATGGAGCACCACATGGCTGAGAG 1426 | GGCGCCTCTTGCAAAGAACATCGTCAGACTCGCAAGCCACGCCGAGCAGAGGGGTCTCCAT 1366 | CACGGAGATCGTCCTGGACGGCTCGACTGGCČTTCTGCATCCTGCTGGGAAGGÁGGGCGT 1306 | GATAACAATTGAAGCAATGGCATTCAAGTTGCCAGTATTGGGCACGGCTGCTGGAGGGAC 1246 | CTTGGCAGCAATTGATGTGCTTGTTCAGAATTCTCAGGGCCGTGGAGAATGCTTTGGAAG 1186 | GAAGAACACGATTCATGACCGTGTCCATTTTGTGAACAAGACATTGGCAGTGGCCCCTTA 1126 | TGTGGGAAGTGATGGTAATGCTCAGACCAAATTTGAGACTCAGTTACGTGACTTTGTGGT 1066 | TCAGGCTTTGCAGCTCATCCAACACGAGAAACTTAAAGTGCCTAGAATACATGCTGTAGT 1006 | GCAATAATAAACAGTGTATCAC-GAGGAAAGGGACAAGACTTATTTCTTCAAGCATTTTA 946 |

Sudman, M. and Pratt

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                                                                       BQ148371
NF067P07FL1F1063 Developing flower
NF067F07FL 5', mRNA sequence.
BQ148371
BQ148371.1 GI:20285430
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                     barrel medic.
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Seq primer: JEN REV
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Fax: 706 583 0210
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/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
a 107 c 123 g 109 t
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/db_xref="taxon:132711"
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Pred. No. 5.4e-93;
0; Mismatches 19;
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809 TGAAGACAATGTCGCAAGAAGAGTCCTTACGGGAACATATTCGTGAATCCCTTTGGAGTACG
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869 GAGTGAGGATCTCCTGTTTGCAATAATAAACAGTGTATCACGAGGAAAAGGGACAAGACTT
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
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Insert Length: 685 Std Error: 0.0
Plate: 067 row: F column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
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/db xref="taxon:3880"
/clone_lib="Npeveloping flower"
/clone_lib="Npeveloping flowers"
/tissue_type="Developing flowers"
/tissue_type="Developing flowers"
/tissue_type="Developing flowers"
/tissue_type="Developing flowers"
/tissue_type="Developing flowers"
/tissue_type="Developing flowers and flowers and flowers and flowers and flowers in early transition into pods."
/note=""Mector: Lambda Zap; cDNA was prepared from polyA+enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing CDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XLI-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

3 others
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Pred. No. 3.2e-91;
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| TCACACAC 641 641 641 641 61 | TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library JOURNAL Unpublished (2001) COMMENT Contact: May GD Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7380 Email: 9dmay@noble.org Email: 9dmay@noble.org Insert Length: 641 Std Error: 0.00 Plate: 050 row: A column: 09 | DN BI271361 GI:14879765 BI271361.1 GI:14879765 S EST. S EST. Medicago truncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; T Spermatophyta; Magnoliophyta; eudicotyledons; core eud Spermatophyta; Magnoliophyta; eudicotyledons; core eud Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae Medicago I (bases I to 641) Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. | 1169 TGGAGAATGCTTTG 1182 | Qy 929 ATTTCTTCAAGCATTTTATCAGGCTTTTGCAGCTCATCCAACACGAGAAACTTAAAGTGCC 988 |
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Fax: 516-344-3407
Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
                                                                                                                                  AGACCAAATTTGAGACTCAGTTACGTGACTTTGT
                                                                                                                                                                                 ACGAGAAACTTAAAGTGCCTAGAATACATGCTGCTAGTTGTGGGAAGTGATGTTAATGCTC
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                                                                                                              AAACAAAGTTTGAAACAGAGCTGCGTAACTTTGT
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/cultivar="Acala Maxxa"

/cultivar="taxon:3635"

/clone lib="Six-day Cotton fiber"

/tissue_type="immature fiber"

/dev_stage="Six days post anthesis"

/lab_host="Xi1-Blue"

/not="Vector: pBluescript II KS+"

/not="Vector: pBluescript II KS+"
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Pred. No. 2.8e-82;
0; Mismatches 171;
                                   375 bp
embryo
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                                  mRNA linear EST 30-M
from Delaware Zea mays cDNA,
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AUTHORS
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Query Match
Best Local Similarity
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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855 California Ave,
Tel: 650 723 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize ESTs from various
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                                       TAAAAGCTGATCTGG
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/dev_stage="14, 21, 20, 30 and 35 days after pollination"
/dev_stage="14, 21, 20, 30 and 35 days after pollination"
/lab_host="E.coli SOLR"
/hote="Organ: embryo; Vector: pBluescript SK, Site 1: XhoI
/ Site 2: EccRI; Library was prepared by Statagene using
the Uni-Zap XR system (Stratagene BN937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
1890s a 104 c 111 g 77 t
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/cultivar="Illinois High Oil"
/db xref="taxon:457"
/clone_lib="687 - Early embryo from Delaware"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Pred. No. 1.1e-77
0; Mismatches 1
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| Qy 1157 TTC | Db 182 TG | Qy 1097 TG | Db 122 GT7 | Qy 1037 ATT | Qy 977 ACT Db 62 GTT | Db 2 GG | Query Match Best Local & Matches 368 | BASE COUNT ORIGIN | | | Institution Tel: Ocerem Tel: O | JOURNAL Unpubl: | | SOURCE Hord ORGANISM Hord Euka Spen | N BQ46 | RESULT 15 BQ464581 LOCUS DEFINITION HF02 |
|---|--|---|--|---|---|---|--|--|---|--|--|--|--|---|--------|---|
| TTCTCAGGGCCGTGGAGAATGCTTTGGAAGGATAACAATTGAAGCAATGGCATTCAAGTT 1216 | TGTCAACAAGACGTTGGCAGTGGCACCTTATTTGGCTGCAATTGATGTGCTTGTCCXGAA 241 | TGAACAAGACATTGGCAGTGGCCCCTTACTTGGCAGCAATTGATGTGCTTGTTCAGAA 1156 | GTTTGAGACACAGTTACGTGAATTTGTGGCGAAGAATGGGATCCATGACCGTGTTCACTT 181 | TTGAGACTCAGTTACGTGACTTTGTGGTGAAGAACACGATTCATGACCGTGTCCATTT 1096 | ACTTAAAGTGCCTAGAATACATGCTGTAGTTGTGGGAAGTGATGTTAATGCTCAGACCAA 1036 | GGGACARGACTTATTCTTCAAGCATTTTATCAGGCTTTGCAGCTCATCCAACACGAGAA 976 | 19.2%; Score 327.2; DB 14; Length 437; Similarity 84.4%; Pred. No. 9.7e-74; Similarity 0; Mismatches 68; Indels 0; Gaps 0; | is NOT oning. To or shou to the ombinats op" | 513" yopsis" poing caryopsis, 16-25 DAF (da: old" luescript SK+; Site_1: EcoRI (luescript SK+; Site_1: EcoRI (col (3'-end of cDNA); developing affer flowing Due to developing | Location/Qualifiers 1437 /organism="Hordeum vulgare" /cultivar="Harke" | ute 394 394 Et Le | mariey Esis from developing seeds Unpublished (2002) Contact: Stein Nils | , Hordeum. to 437) Zhang,H., Weschke,W., Potokina,E. and | Hordeum vulgare. Hordeum vulgare Hordeum vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae | j., | BQ464581 437 bp mRNA linear EST 30-MAY-2002 HF02L01r HF Hordeum vulgare cDNA clone HF02L01 5-PRIME, mRNA |

| | Search completed: July 4, 2003, 22:05:50 Job time : 1711 secs | Sea Job |
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| | 422 TGCGAGCCATGTTGAG 437 | DЬ |
| | 1337 CGCAAGCCACGCCGAG 1352 | Ş |
| 421 | 362 CCTTCTGCACCCTGCTGGAAAGGAGGGCGTCACGCCTCTCGCCAGGAACATGGTAAGGCT 421 | Db |
| 1336 | 1277 CCTTCTGCATCCTGCGAAGGAAGGAAGGAGGGCGTGGCGCTCTTGCAAAGAACATCGTCAGACT 1336 | Ş |
| 361 | 302 GCCAGTGCTGGGTACGGCTGCTGGAGGGACCACCGAAATCGTCTTGGATGGTTCAACCGG 361 | Db |
| 1276 | 1217 GCCAGTATTGGGCACGGCTGCTGGAGGGACCACGGAGATCGTCCTGGACGGCTCGACTGG 1276 | Ş |
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and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Herbicidally activ
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Arabidopsis thalia
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| idisation assay; genetic mapping; gene (ination sequence.) idopsis thaliana. 33405-A2. EP-2000; 2000EP-0301439. EB-2000; 2000EP-0301439. EB-1999; 99US-0121825. AR-1999; 99US-0123180. AR-1999; 99US-0123548. AR-1999; 99US-0125788. AR-1999; 99US-0126264. PR-1999; 99US-0126746. PR-1999; 99US-0126746. PR-1999; 99US-012674. PR-1999; 99US-0128674. PR-1999; 99US-0128674. PR-1999; 99US-0128674. PR-1999; 99US-0128674. PR-1999; 99US-0128674. PR-1999; 99US-0128674. PR-1999; 99US-0128674. | AG28811; 7-OCT-2000 (first entry) rabidopsis thaliana protein fragment SEQ ID NO: 34169 rebin identification; signal transduction pathway; mybridisation assay; genetic mapping; gene expression ermination sequence. rabidopsis thaliana. p1033405-A2. | ALIGNMENTS SULT 1 G28811 AAG28811 standard; Protein; 457 AA. | 11 157 6.5 403 21 AAG24139 11 153.5 6.4 368 22 AAB22953 11 152.5 6.4 368 22 ABB22967 15 152.5 6.4 368 22 ABB22967 16 150 6.3 387 22 AAB96238 17 134.5 5.6 416 22 AAB96238 18 134.5 5.6 416 22 AAB96238 20 134.5 5.6 416 22 AAB96224 21 134.5 5.6 416 22 AAB96268 21 134.5 5.6 416 22 AAB96268 22 133.5 5.6 416 22 AAB96268 23 133.5 5.6 416 22 AAB96268 24 133.5 5.6 416 22 AAB96268 25 133.5 5.6 416 22 AAB96268 26 133.5 5.6 416 22 AAB96268 27 130.5 5.4 409 22 AAB96298 28 129.5 5.4 335 22 AAB96278 29 128.5 5.4 337 22 AAB96278 30 128.5 5.4 335 22 AAB96278 31 127 5.3 381 22 AAB96298 31 127 5.3 381 22 AAB96298 32 128.5 5.2 336 12 AAB76298 33 128.5 5.2 336 12 AAB76298 34 128.5 5.2 384 18 AAW22175 34 128.5 5.2 336 12 AAB76298 37 124.5 5.2 367 21 AAW23778 38 123.5 5.2 367 21 AAW23778 39 123.5 5.2 367 21 AAW3379397 42 111 4.6 323 22 AAW39379 |
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   The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                          Claim 5;
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Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herbicidally active polypeptide
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organisms
                                                                                                                                           Tietjen K, Weidler
                                                                                                                                                                                                                         28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                   28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                                                                                                   WO200210210-A2
                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                     (FARB ) BAYER AG
                                                                                                        2002-269010/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPFVAGAMIDSHTTAEYWNSRTSDRLKIQMPQTYVVHLGNSKELMEVAEDNVARRVLREH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGQKAVDTSLKADLIVLNTAVAGKWLDAVLKENVVKVLPKILWWIHEWRGHYFNADLVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVKEMFMEHHMAERIAAVLKDVLRKSQ 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFKLPVLGTAAGGTMEIVVNGTTGLLHSAGKEGVIPLAKNIVKLATQVELRLRMGKNGYE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFKLEVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYG 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQTKFETQLRDFVVKNTIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAM
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SEQ ID NO 1542; 261pp + Sequence Listing; English

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Matches
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            WPI; 2002-269010/31
                                   Tietjen K,
                                                                                 28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                     WO200210210-A2
                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                 Herbicidal; plant; agriculture; herbicide
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                                                          (FARB ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 TSDRLKIQMPQTYVVHLGNSKELMEVAEDNVA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 PVLKDHVPKVLPKILWWIHEMRGHYFK-----VEYVKHLPFVAGAMIDSHTTAEYWNS-R 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 CDGRGDPAALNTAVASGSPLGFMR---SKLVLLVSHELSLSGGPLLLMELAFLLRHVGSQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                               GRVKEMFMEHHMAERIAAVLKDVLR 465
                                                                                                                                                                                                                                                                                                                                                                                                                             MAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGY 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KVAYVKEMLSFLSNNGNLSNSVLWTPATTRVASLYSAADVYVTNSQGVGETFGRVTIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQTKFETQLRDFVVKN-TIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPRIHAV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEDHVKLR-SQPVIVPLSVNDELAFVAGVSSSLNTPTLTQETMKEKRQKLRESVRTEFGL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYM-DHHPAGGSQIAWWVMENRREYFDRAKPVLDRVKLLIFL----SEVQSKQWLTWC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYAVVLSRRG-----GLLQELTRRRIKVVEDKGELSFKTAMKADLVIAGSAVCASWID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVWITNORSQETNDVTYSLEHRMLNHGVQVLPARGQEAVDIALKADLVILNTAVAGKWLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDRKSD-----FKRLVWSRRFVLLFHELSMTGAPISMMELASELLSCGAT 267
                                                                                                                                                                                                                                                                                                                                                         EIVEKMYMKQHMYKRFVDVLVKCMR
                                                                                                                                                                                                                                                                                                                                                                                                      MAYGLPVLGTDAGGTKEIVEHNVTGLLHPVGRAGNKVLAQNLLFLLRNPSTRLQLGSQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSARHRLRGSSRKMKITSPAVDNHPSVLSATGRRKLLLSGNVTQKQDLKLLLGSVGSKSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDKDMLVMSLSSINPGKGQLLLLESVALALEREQTQEQVAKRNQSKIIKNLNGIRKEKIS 492
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                                   Weidler
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29.1%;
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Pred. No. 7.5e-
77; Mismatches
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'.5e-41;
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RESULT 6
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31-MAY-2002

(first

entry)

ABB91331;

ABB91331 standard; Protein;

670

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Arabidopsis thaliana.

Herbicidal; plant; agriculture; herbicide

Herbicidally active polypeptide

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Best Local S
Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying target proteins (ABB90790-ABB901016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 541; 261pp + Sequence Listing; English
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643
                                 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as herbicides.
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                                                                   EAMAYGLAVVGTDAGGTKEMVQHNMTGLLHSMGRSGNKELAHNLLYLLRNPDERLRLGSE 642
                                                                                                                                                                        DVNAQTKFETQLRDFVVKNTIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITI 378
                                                                                                                                                                                                                                                                                       LNTPTLSPEKMRVKRQILRESVRTELGITDSDMLVMSLSSINPTKGQLLLLESIALALSE 462
                                                                                                                                                                                                                                                                                                                                                                                              VEYVKHLPFVAGAMIDSHTTAEYWNS-RTSDRLKIQMPQTYVVHLGNSKELMEVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 DKGELSFKTAMKADLIIAGSAVCTSWIDQYMNHH-PAGGSQIAWWIMENRREYFDRAKPV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARGQEAVDIALKADLVILNTAVAGKWLDPVLKDHVPKVLPKILWWIHEMRGHYFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIFHELSMTGAPISMMELASELLSCGATVSAVVLSRRG-----GLMQELSRRRIKVVE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVSHELSLSGGPLLLMELAFILRHVGSQVVWITNQRSQETNDVTYSLEHRMLNHGVQVLP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATYGKLLGPFGSLEDKVLEWSPHRRSGTCDRKSD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STAGFILLR--GALRD-----PCDGRGDPAALNTAVASGSPLGFMR---SKLVL
                                                                                                    EAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEK 438
                                                                                                                                         KSNKVGYVKEMLSFLSNSGNLSKSVMWTPATTRVASLYSAADVYVTNSQGVGETFGRVTI
                                                                                                                                                                                                                                                                                                                                                           LDRVKMLIFL-----SESQSRQWLTWCEEEHIKLR-SQPVIVPLSVNDELAFVAGIPSS
GRKMVEKMYMKQHMYKRFVDVLVKCMR
                               GYGRVKEMFMEHHMAERIAAVLKDVLR
                                                                                                                                                                                                                 RGQESQRNHKGIIRKEKVSLSSKHRLRGSSRQMKSVSLTLDNGLRREKQELKVLLGSVGS
                                                                                                                                                                                                                                                                                                                      -----EDNVARRVLREHIRESIGVRSEDLLFAIINSVSRGKGODLFLQAFYQALQ- 299
                                                                                                                                                                                                                                                -----LIQHEKLKVPRIHAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 482.5; DB 23;
Pred. No. 2.1e-40;
7; Mismatches 173;
 669
                                  465
                                                                                                                                                                                                                                                    -----VVGS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----FKRLVWSRRFV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        670;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-2001;
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                   GYGRVKEMFMEHHMAERIAAVLKDVLR
                                                            EAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEK
                                                                                                                                                                                                                                                              ARGOEAVDIALKADLVILNTAVAGKWLDPVLKDHVPKVLPKILWWIHEMRGHYFK-----
                                                                                                                                                                                                                                                                                                    LVSHELSLSGGPLLLMELAFLLRHVGSQVVWITNQRSQETNDVTYSLEHRMLNHGVQVLP
                                                                                                                                                                                                                                                                                                                          ATYGKLLGPFGSLEDKVLEWSPHRRSGTCDRKSD------
                                                                                                                                                                                                                                                                                                                                             STAGFLLR--GALRD------PCDGRGDPAALNTAVASGSPLGFMR---SKLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 542;
     GRKMVEKMYMKQHMYKRFVDVLVKCMR
                                                                                KSNKVGYVKEMLSFLSNSGNLSKSVMWTPATTRVASLYSAADVYVTNSQGVGETFGRVTI
                                                                                                  DVNAQTKFETQLRDFVVKNTIHDRVHFVNKTLAVAFYLAAIDVLVQNSQGRGECFGRITI
                                                                                                                       RGQESQRNHKGIIRKEKVSLSSKHRLRGSSRQMKSVSLTLDNGLRREKQELKVLLGSVGS
                                                                                                                                                               LNTPTLSPEKMRVKRQILRESVRTELGITDSDMLVMSLSSINPTKGQLLLLESIALALSE
                                                                                                                                                                                 -----EDNVARRVLREHIRESLGVRSEDLLFAIINSVSRGKGQDLFLQAFYQALQ-
                                                                                                                                                                                                       LDRVKMLIFL-----
                                                                                                                                                                                                                         VEYVKHLPFVAGAMIDSHTTAEYWNS-RTSDRLKIQMPQTYVVHLGNSKELMEVA-----
                                                                                                                                                                                                                                            DKGELSFKTAMKADLIIAGSAVCTSWIDQYMNHH-PAGGSQIAWWIMENRREYFDRAKPV
                                                                                                                                                                                                                                                                                   LIFHELSMTGAPISMMELASELLSCGATVSAVVLSRRG-----GLMQELSRRRIKVVE
                                                                                                                                                                                                                                                                                                                                                                                                        670 AA;
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                           -LIQHEKLKVPRIHAV-----
                                                                                                                                                                                                                                                                                                                                                                          20.1%;
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                                                                                                                                                                                                      SESQSRQWLTWCEEEHIKLR-SQPVIVPLSVNDELAFVAGIPSS
                                                                                                                                                                                                                                                                                                                                                                          Score 482.5; DB 2
Pred. No. 2.1e-40;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
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     669
                                        LHSMGRSGNKELAHNLLYLLRNPDERLRLGSE
                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                                                                                                 173;
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Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                  specification, at ftp.wipo.int
                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form specification, but was obtained in electronic i at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic a
genes from Drosophila
interactions -
                                                                                                                                                                                                                                                                                                                                                                   Sequence
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                              HGVQVLPARGQEAVDIALKADLVILNTAVAGKW-----LDPVLKDHVPKVLPKILWWI
                                                                                                                                                                                                                      VLFLHPDLGIGGAERLVVDAALALKERGHQVSFLTNHHDSTHCFKETADGTFPV-----
                                                                                                                                                                                                                                                         VLLVSHELSLSGGPLLLMELAFLLRHVGSQVVWITNQRS-----QETNDVTYSLEHRMLN
                                     SKELMEVAEDNVAR----RVLR----
                                                                          LRFAPHRPKVLFYCHFP.
                                                                                                          HEMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLKIQMPQTYVVHLG----
                                                                                                                                             HVVGDWLPRGLFGRFYAICAYLRMLYAAIYASFFMPQREQVDVVVCDLISVCIP-----V
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2000US-0614150.
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                                                                                                                                                                                                                                                                                          Score 179.5; DB 22
Pred. No. 2.1e-09;
'3; Mismatches 181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capsular gene cluster; serotype 2; polysaccharide biosynthesis; capsular component; antigen; regulation; chain length determination; complement-mediated opsonophagocytosis; serotype-specific detection; antigen; vaccine; Streptococcal disease; ORF 2Z; ORF 2Z; ORF 2Z; Cps2B; Cps2B; Cps2C; Cps2D; Cps2E; Cps2F; Cps2G; Cps2H; Cps2I; Cps2J, Cps2C; Cps2O; Cps2O; Cps2N; Cps2C; Cps2O; C
The proteins AAY68950-69 are encoded by the capsular gene cluster of Streptococcus suis serotype 2. The genes in this cluster are involved in polysaccharide biosynthesis of capsular components and antigens. The proteins are involved in regulation (CpsA), chain length determination (CpsB, CpsC), export (CpsC), and biosynthesis (CpsE, CpsF, CpsG, CpsH, CpsJ, CpsC). The capsule confers bacterium resistance to complement-mediated opsonophagocytosis. The gene cluster is used as a source of probes and primers for serotype-specific detection of S. suis and is also useful for recombinant production of the proteins. The proteins are then useful for producing antigens that can be used in vaccines, for controlling or eradicating a Streptococcal disease, in
                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid containing the capsular gene cluster of Streptococcus suis, used for serotype-specific detection and to generate antigens or mutants for vaccination
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22-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 3; 144pp; English.
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98EP-0202467.
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09-WAR-1999

23-WAR-1999

25-WAR-1999

29-WAR-1999

01-APR-1999

06-APR-1999

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16-APR-1999

19-APR-1999

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                      Protein identification; signal transduction hybridisation assay; genetic mapping; gene etermination sequence.
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                                                                                                                                                                                                                                                                                         HFV-----NKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGT 395
                                                                                                                                                                                                                                                                                                                                     LAVSAF----AILCKHKONLSDVTLTVAGKCGYDERLKENVEYLEELRSLAEKEGVSDRV
                                                                                                                                                                                                                                                                                                                                                         LFLQAFYQALQLIQHEKLKVPRIHAVVVG----SDVNAQTKFETQLRDFVVKNTIHDRV
                                                                                                                                                                                                                                                                                                                                                                                  AQGSRPAVLYPA--------VNIDQFIEPHTYKLNFLSINRFERKKNID
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                                                                                                                                                                                              KLNOYLVDVVSSPKE
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                                                                                          (first entry)
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99US-0167741.
99US-0160767.
99US-0160768.
99US-0160814.
99US-0160814.
99US-0160980.
99US-0160981.
99US-0161406.
                                                                                                                                      Protein; 397
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Pred. No. 1.6e-07;
4; Mismatches 186,
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                                                                     SEQ ID NO: 53858.
                                    expression
                                    pathway; metabolic
expression control;
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                                   pathway;
promoter;
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05-MAR-1999;
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330 KNGVTGYLCEPTPEDFSSAMA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 6.6%; Score 157.5; DB 21; Length
Similarity 21.8%; Pred. No. 3.6e-07;
94; Conservative 74; Mismatches 186; Indels
                               LDGSTG-LLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAERIAA
                                                                          RPAVLYPA-----VNIDOFIEPHTYKLNFLSINRFERKKNIDLAVS
                                                                                                                                                                                                                                                                  QTYVVHLGNSKELMEVAEDNVARRVLREHIRESLGVRSEDLLFAIINSVSRGKGQDLFLQ : |: : | | | | | | | | | | :
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                                                                                                                                                                                                                                                                                                                                                                                                         FLPRHIFYRLHAVCAYLRCLFVALCVLLGWSSFDVVLADQVSVVVPLLKLKRSSKVVFYC
                                                                                                                                                                                                                                                                                                                                                                                                                                  VLPAR---GQEAVDIALKADLVILNTAVAGKWLDPVLKDHVPKVLP-----KILWWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLLVSHBLSLSGGPLLLMELAFILRHVGSQV-VWITNQRSQETNDVTYSLBHRMLNHGVQ
                                                                                                                                                             AF----AILCKHKONLSDVTLTVAGKCGYDERLKENVEYLEELRSLAEKEGVSDRVNFIT
                                                                                                                                                                                      AFYQALQLIQHEKLKVPRIHAVVVG-----SDVNAQTKFETQLRDFVVKNTIHDRVHFV-
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99US-0161360

99US-0161361

99US-0161393

99US-0161993
-RFIENPELANRMGAEARNHVVESFSVKTFGQKLNQ
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                                      458
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Query Match
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96; Conserv
 HGVQVLPAR----GQEAVDIALKADLVILNTAVAGKWLDPVLKDHVPKVLP------KI
                                                       SKMNIAIIHPDLGIGGAERLIVDAAVELASHGHKVHIFTSHHDKSRCFEETLSGIFQVTV 66
                                                                               SKLVLLVSH-ELSLSGGPLLLMELAFLLRHVGSQV-VWITNQRSQETNDVTYSLEHRMLN 133
                                                                                                                                6.5%;
nilarity 22.2%;
Conservative 7:
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Pred. No. 4.2e-07;
4; Mismatches 187;
                                                                                                                                                                  Length 403;
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                       182
 RESULT 12
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| 99US-014484 99US-0144814 99US-0145086 99US-0145085 99US-0145087 99US-0145087 99US-0145192 99US-0145192 99US-0145192 99US-0145118 | 99US-0144331 99US-0144331 99US-0144332 99US-0144333 99US-0144334 99US-0144352 99US-0144352 | 99US-0136021 99US-0136392 99US-013782 99US-0137502 99US-0137502 99US-0138540 99US-0138540 99US-0139452 99US-0139453 99US-0139453 99US-0139455 99US-0139456 99US-0139456 99US-0139456 99US-0139461 99US-0139461 99US-0139461 99US-0139462 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0143543 99US-014353 99US-0143543 | 99US-0134219 99US-0134221, 99US-0134370, 99US-01343768, 99US-0134941, 99US-0135124, 99US-0135123, 99US-0135353, |
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ID AAY93
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                                                                                                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                          Virulence protein; tatA; tatB; tatC; tatE; r
eckl; iroD; iroC; iroE; mtd2; ms1; vaccine;
                                                                                                                                                                                                                                                                                                                                          An Escherichia coli virulence
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milarity 21.7%;
Conservative 7
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  98GB-0024569.
98GB-0024570.
98GB-0027814.
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99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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99US-0161405.
99US-0161406.
99US-0161359.
                                                                                       99WO-GB03721
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; Pred. No. 9.3e-07;
74; Mismatches 187;
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                                                                                                                                                                                                                                                                            mdoG; creC;
; infection;
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RESULT 1,
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17-DEC-1998;
17-DEC-1998;
17-DEC-1998;
13-JAN-1999;
13-JAN-1999;
28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents an Escherichia coli virulence protein. The specification describes virulence proteins which are encoded by an operon including tatk, tatB, tatC, tatB, mdoG, creC, recG, yggN, eckl, iroD, iroC, iroE, mtd2 or ms1-16 genes obtained from Escherichia coli KI. The virulence proteins and polymucleotides, and their vaccines are useful for screening potential drugs, for the detection of virulence, and for treating or preventing conditions associated with infection by a Gram negative bacterium particularly Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide encoded by an operon including genes from Escherichia coli for screening potential drugs, detecting virulence and treating conditions associated with infection by a Gram negative bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2;
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DB; AAA15182.
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GGVREVI - - GDDDFLVPISDS - - TQLASKIEKL - SLSQIRDHIGFRNRERILKNF
                         GGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMF 447
                                                     LIKKLQLSNRVSLLGVKKNIAPYFSACDIFVLSS--RWEGFGLVVAEAMSCERIVVGTDS
                                                                              FVVKNTIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAA
                                                                                                           AAGRLTLAKDYPNLLNAM---TLLPEHFKL-
                                                                                                                                  IINSVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVGSDVNAQTKFETQLRD----
                                                                                                                                                                  SKEAVDEFLRIKAFNP-AKAITMYNGIDTNKFKFDLLARR----EIRDGINIKNDDILLL
                                                                                                                                                                                                                       ----VHSHMFHANIITRLSVIGIKNRPGIISTAHNKNEGGYFRMLTYRITDCLSDCCTNV
                                                                                                                                                                                                                                                  WIHEMRGHYFKVEYVKHLPFVA----GAMIDSHTTAE--YWNSRT-----SD-----
                                                                                                                                                                                                                                                                             FPSE-----NNVNVINVNMSKNISGVIKGCVRI------RDVIANFKPDI--
                                                                                                                                                                                                                                                                                                     YSLEHRMLNHGVQVLPARGQEAVDIALKADLVILNTAVAGKWLDPVLKDHVPKVLPKILW
                                                                                                                                                                                                                                                                                                                                  VITGLGLG-GAEKQVCLLADKLSLSGHHVKIISLGHM---
                                                                                                                                                                                                                                                                                                                                                              VASGSPLGFMRSKLVLLVSHELSLSGGPLLLMELAFLLRHVGSQVVWITNQRSQETNDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 66-67; 122pp; English.
                                                                                                                                                                                          -----RLKIQMPQTYVVHLGNSKELMEVAEDNVARRVLREHIRESLGVRSEDLLFA
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                                                                                                                                                                                                                                                                                                                                                                                      Score 152.5; DB 21;
Pred. No. 1.1e-06;
8; Mismatches 150;
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                                                                                                           -----IIIG-----DGELRDEINM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
systemic infection; non-diarrhoeal infection; septicaemia;
pyelonephritis; antibiotic resistance.
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02-FEB-2001; 2001FR-0001449
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                                                                                                                                                                                                      185 WIHEMRGHYFKVEYVKHLPFVA----GAMIDSHTTAE--YWNSRT-----SD-----
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                                                                                                                                                                                                                                                                                                                               VASGSPLGFMRSKLVLLVSHELSLSGGPLLLMELAFLLRHVGSQVVWITNQRSQETNDVT
SKEAVDEFLRIKAFNP-AKAITMYNGIDTNKFKFDLLARR----EIRDGINIKNDDILLL
                                                                                                                                                                         ----VHSHMFHANIITRLSVIGIKNRPGIISTAHNKNEGGYFRMLTYRITDCLSDCCTNV
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                                                                            IINSVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVGSDVNAQTKFETQLRD----
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Pred. No. 1.1
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                                                 -DGELRDEINM
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02-FEB-2001; 2001FR-0001449.
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FPSE----NNVNVINVNMSKNISGVIKGCVRI---
                                                                                  VASGSPLGFMRSKLVLLVSHELSLSGGPLLLMELAFLLRHVGSQVVWITNQRSQETNDVT 124
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ilarity 21.7%;
Conservative 6
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                                                                                                               Score 152.5; DB 22,
Pred. No. 1.1e-06;
8; Mismatches 150;
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   --RDVIANFKPDI--
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| plet 74 | 296 | 393 | 238 | 333 | 197 | 277 | 142 | 226 | 98 | 185 |
| Search completed: June 30, 2003, 16:26:51 Job time : 74 secs | 296 GGVREVIGDDDFLVPISDSTQLASKIEKL-SLSQIRDHIGFRURERILKNF 345 | GGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMF 447 | 238 LIKKLQLSNRVSLLGVKKNIAPYFSACDIFVLSSRWEGFGLVVAEAMSCERIVVGTDS 295 | 333 FVVKNTIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLFVLGTAA 392 | 197 AAGRLTLAKDYPNLLNAMTLLPEHFKLIIIGDGELRDEINM 237 | LKVPRIHAVVVGSDVNAQTKE | 142 SKEAVDEFLRIKAFNP-AKAITMYNGIDTNKFKFDLLARREIRDGINIKNDDILLL 196 | 226RLKIOMPQTYVVHLGNSKELMEVAEDNVARRVLREHIRESLGVRSEDLLFA 276 | 86VHSHMFHANIITRLSVIGIKNRPGIISTAHNKNEGGYFRMLTYRITDCLSDCCTNV 141 | 185 WIHEMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSD 225 |

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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US-08-597-236-8
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US-09-403-768-8
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US-08-91-445A-5
US-08-93-433A-10
US-09-323-433A-10
US-09-356-499-5
US-09-568-102-5
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                                                                                                                                                                                       CLASSIFICATION: 426
PRIOR APPLICATION DATA
PPLICATION NUMBER: EP 95201669.9
PILING DATE: 20-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: protein
US-08-597-236-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-08-597-236-8
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                                                                                                                          Query Match
Best Local S
Matches 69
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: LACTIC BACTERIA PRITITLE OF INVENTION: EXOPOLYSACCHARIDES NIMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
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STATE: Nev
COUNTRY:
                                                                                                                        y Match 5.2%;
Local Similarity 21.8%;
nes 69; Conservative 6;
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T: 1155 Avenue of the Americans
New York
: New York
RY: U.S.A.
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US-08-53-436A-8
US-09-194-905-12
US-08-766-014-4
US-08-756-354-2
US-08-796-414B-1
US-08-796-414B-1
US-08-766-014-3
US-08-766-014-2
US-08-766-014-2
US-09-134-001C-6618
US-09-134-001C-6618
US-09-134-001C-7
US-08-764-101B-7
US-08-484-101B-7
US-08-484-101B-7
US-08-484-101B-7
US-08-488-101B-7
US-09-488-743-22
US-09-697-367-2
                                                                                                                        ;; Score 125.5; DB 1;
;; Pred. No. 0.00013;
62; Mismatches 134;
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                                                                                                                            Indels
                                                                                                                                                            Length 372;
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Sequence 12, Appli
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Sequence 2, Appli
Sequence 4618, Ap
Sequence 7, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
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Result No.

Score

Query Match

Length DB

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Gaps

Minimum Maximum

DB DB

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length: 0 length: 2000000000

Scoring table:

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Title: Perfect score:

US-09-938-294-45 2397

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; MOLECULE TYPE: US-08-746-682A-8
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US-08-746-682A-8
                                                                                                                                                                          Query Match 5.2%; Score 125.5; DB 1; Best Local Similarity 21.8%; Pred. No. 0.00013; Matches 69; Conservative 62; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08746682A Patent No. 5786184 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: ELOPBY disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-NOV-1996
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/597,236
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: BP 95201669.9
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: BP 95201669.9
APPLICATION NUMBER: 30256
THEORMATION NUMBER: 30256
THEORMATION NUMBER: 30256
                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 372 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: STINGELE, FR
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LAC
TITLE OF INVENTION: EXO
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STREET: 1155 Ave
CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                      207
                                                                                                                             151 LKADLVILNTAVAGKWLDPVLKDHVPKV-LP-KILWWIHEMRGHYFKVE--YVKHLPFVA
                                                                                     83 INPDIVYLHSTFAG-----VVGRIASIGLPTKVVYNPH---GWSFKMDNSYLKKLIF--
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                                          GAMIDSHTTAEYWNSRTSDRLKIQMPQTYVV--HLGNSKELMEVAEDNVARRVL----RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIBEIF--PNEDFIIGMVGRLSPPKEFFFFIDFAKKILQIRNDTNF-----IIVGDG- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KLIEFSLSFLTDKFILISESEYILANHISFNKSKFSLINNGV--EVITGDSRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1155 Avenue of the Americans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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  --KLIEFSLSFLTDKFILISESEYILANHISFNKSKFSLINNGV--EVITGDSRN 182
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                                                                                                                                                                                                                     Length 372;
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 198-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3206
LENGTH: 387
TYPE: PRT
TYPE: PRT
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US-09-134-001C-3206
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
466 KSQEHSRS 473
                                   322 FIVDIGDSTQA--AKYAIKLLSNPELYQKMQSQMLKDIEARFSSDLITDQYENYYRKMLE 379
                                                                                                                        264 LGKONDVSAFYOLSDLVLLLSE--KESFGLTLLEAMKTGVLPIGSHAGGIKEVIRHEETG
                                                                                                                                                                 346 VNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTG
                                                                                                                                                                                                                                                                                                   162 ----QTYEI-INTKKEIIPIYNFVRENEFPTRHNEELKDCYGISPEEKVLIHVSNFRKVK
                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                              217 RIDTVIETFAKV-----HESIP----SKLILLGDGPELIDMRHKARELDVET----HVLF
                                                                                                                                                                                                                                                      286 GQDLFLQAFYQALQLIQHEKLKVPRIHAVVVGSDVNAQTKFETQLRDFVVKNTIHDRVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                189 MRGHYFKVEYVKHLPFVAGAMID---------
                                                                                                                                                                                                                                                                                                                                             229 IQMPQTYVVHLGNSKELMEV---AEDNVARRVLREHIRESLGVRSEDLLFAIINSVSRGK 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 QEAV------DIALKADLVILNTAVAGKWLDPVLKDHVPKVLPKILWWIHE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 QYAVFQYPPYDITLSTKISDVIQEYDLDILHMHYA------VPHAVCGIL--AKQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 SLSGGPLLLMELAFLLRHVGSQVVWITNQRSQETNDVTYSLEHRMLN---HGVQVLPARG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 5.0%; Score 119; DB 4; 1 Similarity 18.7%; Pred. No. 0.00069; 80; Conservative 77; Mismatches 173;
                                                                              LLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAERIAAVLKDVLR 465
                                                                                                                                                                                                                                                                                                                                                                                      MSGKNVKIMTTLHGTDITVLGYDHTLQNAIKFGIEQSDIVTSVSHSLAQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGRVKEMF-MEHHMAE 454
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RESULT 5
US-08-941-445A-5
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SEQ ID NO 8

SENGTH 373

TYPE: PRT
ORGANISM: Pseudomonas aeruginosa RFaG (WaaG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Applic
Patent No. 6444804
                                                                                                                                                                                                                                         Sequence 5, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Koeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-403-768-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1997-05-0
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: U.S. 60/045,418
PRIOR FILING DATE: 1997-05-02
PRIOR APPLICATION NUMBER: U.S. 60/046,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 6580-177
CURRENT APPLICATION NUMBER: US/09/403,768
CURRENT FILING DATE: 1999-11-02
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COUN'RE.
2IP: 80303
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6444804el Proteins Involved in the Synthesis and TITLE OF INVENTION: of Core Lipopolysaccharide of Pseudomonas Aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Organism: Pseudomonas aeruginosa OTHER INFORMATION: serotype 05 strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 LGLNDQVQILKGRSDIPRFLLGADLLIHPAY--NENTGTVLLEALVSGLPVLVTDVCGYA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 SVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVGSDVNAQTKFETQLRDFVVKNT- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 --IHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 KIQMPQTYVVHLGNSKELMEVAEDNVA--RRV-----LREHIRESLGVRSEDLLFAIIN 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 HYIAEADAGRVLPSPTEODSLNRLLAEMLEDAPARAAWSRNGLAYADHAD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 EIVLDGSTGLLHPAGKE------GVAPLAKNIVRLASHAE 430
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                                                                                                                                   Boulder
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De Kievit, Teresa
Burrows, Lori L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVQQP-LLVKHYGTQAERFHLLPPGISQDRRAPANAADVRAEFRREFGLEEDDLLLVQIG 203
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                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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GENERAL INFORMATION:
APPLICANT: Guarente, Leonard P.
APPLICANT: Austriaco Jr., Nicanor
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determini
TITLE OF INVENTION: in Yeast
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 10, Application US/08861464
Patent No. 5874210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 44; Conservative
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Best Local Similarity 22.8%;
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC COMPS:-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,464
FILING DATE: 22-MAY-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 533 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
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APPLICATION NUMBER: US 60
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 AKALNKEALQAEVGLPVDRNIPLVAFIGRLEEQKGPDVMAAAIPQLMEMVED-----V 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 ARRVLREHIRESLG--VRSEDLLFAIINSVSRGKGQDLFLQAFYQALQLIQHEKLKVPRI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 VTS--RFEPCGLIQLQGMRYGTPCACASTGGLVDTIIEGKTGFHMGRLSVDCNVVEPADV 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 QIVLLGT---GKKKFERMLMSAEEK-----FPGKVRAVVKFNAALAHHIMAGADVLA 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 EGVAPLAKNIVRL 425
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                                                                                                                                                                                                                                                                                                                       E: Hamilton, Brook
Two Militia Drive
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In Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                Brian
Genes Determining Cellular Senescence
in Yeast
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                                                                                                                                                                                                                                                                                                                                                Smith & Reynolds, P.C
                                                                                                                 Version #1.30
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RESULT 7
US-08-396-001-10
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Best Local Similarity
""" Conserva
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                                                                         GENERAL INFORMATION:
APPLICANT: Guarente
APPLICANT: AUSTRIAC
APPLICANT: Claus, (
APPLICANT: Cole, F:
APPLICANT: Kennedy,
                                                                                                                                                                                               Sequence 10, Application US/08396001
Patent No. 5919618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 781-861-9540
INFORMATION FOR SEQ_ID_NO: 10:
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: Genes Determining Cellular Senesence
TITLE OF INVENTION: Yeast
NUMBER OF SEQUENCES: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/I
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 1
FILING DATE: 28-FEB-1
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6408A2Z
TELECOMPUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 508 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                         408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 LVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGT----TEIVLDGSTGLLHPAGKEGVAP 417
                                                                                                                                                                                                                                                                                                                                                             451 -----HMAERIAAVLKDV---LRKSQEHSR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                         418 LAKNIVRLASH-----AEQRVSMGEKG-YGRVKEMFMEH------------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 EKLKVPRIHAVVVGSDVNAQTKFETQLRDFVVKNTIHDRVHFVNKTLAVAPYLA--AIDV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 --AVVYLAHTH--DGARVAMHC---LWHGTPKDRKVIVKTMKTYVEKVANGQYSHLVLLA 266
                                                                                                                                                                                                                                                                                                                     465 SLLQSCDLEVANKVKAALKSLIPTLEKTKSTSK 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 YFKVEYVKHLPFVAGAMIDSHTTAEYMNSRTSDR-LKIQMPQTYVVHLGNSK--ELMEVA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 IMDEMKQILTPMAQK-EAVIKHSLVHKVFLDFFTYAP-----PKLRSEMIEAIRE---- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AVD------IALKADLVILNTAVAGKWLD-----PVLKDHVPKVLPKILWWIHEMRGH 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 MLRHAEASAIVEYAYNDKAILEORNMLTEELYGNTFOLYKSADHRTLDKVLEVOPEKLEL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 LLRHVGSQVV------WITNQRSQETNDV---TYSL----EHRMLNHGVQVLPARGQE 145
                                                                                                                                                                                                                                                                                                                                                                                                 IAEH----PAGHLVLKWLIEQDKKWKENGREGCFAKTLVEHVGMKNLKSWASVNRGAIILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EIIEVLOKGDGNAHSKKDTEVRRELLESI-----SPALLSYLOEHAQEV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFDCIDDTKLVKQIIISEIISSLP-----SIVND-KYGRKVLLYLLSPRDPAHTVR- 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EDNVARRVLREHİREŞIGVRSEDLLFAİINSVSRGKGQDLFLQAFYQALQLIQH 303
                                                                                      Austriaco Jr., Nicanor
Claus, James
Cole, Francesca
                                                                                                                                                       Guarente, Leonard P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/107,408
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4.4%; Score 105.5; DB 2; Length 508;
Best Local Similarity 21.4%; Pred. No. 0.029;
Matches 97; Conservative 75; Mismatches 140; Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 508 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REGERRENCE/DOCKET NUMBER: MIT-6408A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook
STREET: Two Militia Drive
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Mil:
CITY: Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                               408 IAEH----PAGHLVLKWLIEQDKKMKENGREGCFAKTLVEHVGMKNLKSWASVNRGAIILS
                                                                                                                                                                                                          362 LYQNSQGRGECFGRITIEAMAFKLPVLGTAAGGT----TEIVLDGSTGLLHPAGKEGVAP 417
                                      451 -----HMAERIAAVLKDV---LRKSQEHSR 472
                                                                                                                        418 LAKNIVRLASH-----AEQRVSMGEKG-YGRVKEMFMEH-------
                                                                                                                                                                 362 VLDKS-----ACVLVSDILGSATGDVQPTMNAIASLAATG-LHPGGKDGELH 407
                                                                                                                                                                                                                                                  317 -----SPALLSYLQEHAQEV
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465 SLLOSCDLEVÁNKVKÁALKSLIPTLEKTKSTSK 497
                                                                                                                                                                                                                                                                                         304 EKLKVPRIHAVVVVGSDVNAQTKFETQLRDFVVKNTIHDRVHFVNKTLAVAPYLA--AIDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 MLRHAEASAIVEYAYNDKAILEQRNMLTEELYGNTFQLYKSADHRTLDKVLEVQPEKLEL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 IMDEMKQILTPMAQK-EAVIKHSLVHKVFLDFFTYAP-----PKLRSEMIBAIRE----
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RESULT 8
US-09-323-433A-10
; Sequence 10, Application US/09323433A
; Patent No. 6218512
; GENERAL INFORMATION:

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RESULT 9
US-09-335-409-5
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PRIOR APPLICATION NUMBER: US 08/107,408
PRIOR FILING DATE: 1993-08-16
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 3
SEQ ID NO 10
                                                                                                                                               Sequence 5, Application US/09335409
Patent No. 6121029
GENERAL INFORMATION:
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APPLICANT: Cole, Francesca
APPLICANT: Cole, Francesca
APPLICANT: Kennedy, Brian
TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
TITLE OF INVENTION: YASI
TILLE REFERENCE: 0050.1491-003
CURRENT APPLICATION NUMBER: US/09/323,433A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US/08/396,001
PRIOR APPLICATION NUMBER: US/08/396,001
PRIOR APPLICATION NUMBER: DET/US/09/09351
PRIOR APPLICATION NUMBER: PCT/US/09/09351
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APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
APPLICANT: Gerls, Joern
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TYPE: PRT
ORGANISM: Homo sapiens
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21.4%; Pred. No. 0.029;
ative 75; Mismatches 140;
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                    FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09568102 Patent No. 6346404
                                                                                                                                                                                                                                                            APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
                                                                                                                                                                                           APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
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                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/335,409
; CURRENT FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANIEM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6681 IFATAGTPEKRAWLREQ-----GIAHVMDSRSLDFAEQVLAATKGEGVD------VVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6783 VRRPERVAALLAEVVDLLARGALQPLPVEIFPLSRAADAFRKMAQAQHLGKLVLALEDPD 6842
7005 GNYAAANTFLDALAHHRRAQGLPALSID
                                                                                                                                                                                                                                                                                                                                                                                                                      304 EKLKVPRIHAVVVVGSDVNAQTKFETQLRDFVVKNTIHDRVHFVNKTLAVAPYLA-----
                                                    438 KGYGRVK---EMFMEHHMAERIAAVLKD 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 PAALNTAVASGSPLGFMRSKLVLLVSHELSLSGGPLLLMELAF------LLRHVGSQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V------VWITNORSOETNDVTYSLEHRMLNHGVQVLPARGQEAVDIALKADLVIL 158
                                                                                                                                                                               AAGGTTEIVLDGST------GLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGE 437
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                                                                                                                                                                                                                                                                                                 -----AIDVLVQNSQGRGECFG-RITI------
                                                                                                                 AAGILDDGLLMQQTPARFRAVMAPKVRGALHLHALTREAPLS-FFVLYASGAGLLGSPGQ
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6680

6737

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APPLICANT: Zikle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Gyer, Devon
ITILE Goetlach, Joern
ITILE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPO
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
TYPE: PRT
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; ORGANISM: So
US-09-568-102-5
                                                                                                             ; ORGANISM: Sorangium cellulosum US-09-567-969-5
          Ouery Match 4.4%; Score 104.5; DB 4; Best Local Similarity 19.7%; Pred. No. 3.2; Matches 100; Conservative 61; Mismatches 146;
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Patent No. 6355457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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            Indels
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PRIOR TILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
CREANISM: Sorangium cellulosum
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                                                                                                                                                                    Query Match
Best Local Sin
Matches 100;
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Patent No. 6355458
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
                                                                    6623 PAALTAAQAAALPVAFMTAWYGLV--HLGRLRAGERVLIHSATGGTGLAAVQIARHLGAE 6680
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6681 IFATAGTPEKRAWLREQ-----GIAHVMDSRSLDFAEQVLAATKGEGVD------VVL
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                                                                                                                                                               h 4.4%; Score 104.5; DB 4; Length 7257; Similarity 19.7%; Pred. No. 3.2; 00; Conservative 61; Mismatches 146; Indels 201;
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| Query Match 4.4%; Score 104.5; DB 4; Length 7257; Best Local Similarity 19.7%; Pred. No. 3.2; Matches 100; Conservative 61; Mismatches 146; Indels 201; Gaps 21; 89 PAALNTAVASGSPLGFMRSKLULLVSHBLISLSGGBLLLAMBLAFLLRHVGSQ 108 | 09/568,486 10 35,409 | Qy 391 AAGGTTEIVLDGSTGLIHPAGKEGVAPLAKNIVRLASHAEQRVSNGE 437 | Qy 304 EKLKVPRIHAVVVGSDVNAQTKPETQLRDFVVKNTIHDRVHFVNKTLAVAPYLA 357 | Qy 219 WNSRTSDRLKIQMPQTYVVHLGNSKELMEVAEDNVARRVL-REHIRESLGVRSED 272 Db 6738SLSTLVPDGRFIELGKT | Db 6681 IFATAGTPEKRAMLREQGIAHVMDSRSLDFAEQVLAATKGEGVDVVL 6727 Qy 159 NTAVAGKWLDPVLKDHVPKVLPKILWWIHEMRGHYFKVEYVKHLPFVAGAMIDSHTTAEY 218 |
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| Qy 109 VVWITNQRSQETNDVTYSLEHRMINHGVQVLPARGQEAVDIALKADLVIL 158 | LENGTH: 725 | | 391 6946 438 | 304 EKLKV ::: 6843 VRIRV 358 | Db 6738SISTLVPDGRFIELGKTDIYADRSLGLAHFRKSLSYSAVDLAGLA 6782 Qy 273LLFAIINSVSRGKGQDLFLQAFYQALQLIQH 303 |

| 358AIDVLVQNSQGRGECFG-RITI | Qy 3 Db 68 | |
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| 273 | Qy 2 Db 67 | |
| 219 WNSRTSDRLKIQMPQTYVVHLGNSKELMEVAEDNVARRVL-REHIRESLGVRSED 272 | Db 63 | |
| 159 NTAVAGKWLDPVLKDHVPKVLPKILWWIHEMRGHYPKVEYVKHLPFVAGAMIDSHTTAEY 218 | Qy 67 | |
| 109 VVWITNQRSQETNDVTYSLEHRMLNHGVQVLPARGQEAVDIALKADLVIL 158 | Qy 4d | |
| 58 PAALNTAVASGSPLGEMRSKLVLLVSHELSLSGGELLLMELAFLLRHVGSQ 108 | Qy Db 66 | |
| ery Match 4.4%; Score 104.5; DB 4; Length 7257; st Local Similarity 19.7%; Pred. No. 3.2; ches 100; Conservative 61; Mismatches 146; Indels 201; Gaps 21; | Query Mat Best Loca Matches | |
| JOY EKLEVPRIHAVVOSDWAQTKETQARDFVLKTILAVAPYLA | Qy Qy Qy Qy Db 6 Qy Db 6 Qy Db 6 Qy Db 7 RESULT 15 Sequence Patent N PAPPLICAN APPLICAN |
| RKT.KVDRTHAVAVGSDVNAOTKEETOT DDEVAKOTTUDDVATEVAKOT AVADVT | • | |

| 391 AAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGE 437 | Д | Ş | Db | ρ |
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| AAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSM : : | 7005 | 438 | 6946 | 391. |
| 3E 43 : 3Q 70 | GNYAAANTFLDALAHHRRAQGLPALSID 7032 | KGYGRVKEMFMEHHMAERIAAVLKD 462 | AAGILDDGLLMQQTPARFRAVMAPKVRGALHLHALTREAPLS-FFVLYASGAGLLGSPGQ 70 | 391 AAGGTTEIVLDGSTGLHPAGKEGVAPLAKNIVRLASHAEQRVSMGE 437 |

Search completed: June 30, 2003, 16:31:00 Job time : 29 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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Sequence 22, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 3890, Ap
Sequence 4738, Ap
Sequence 4738, Ap
Sequence 5896, Ap
Sequence 5, Appl
Sequence 107, App
Sequence 107, App
Sequence 296, App
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APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Kachel
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226, AND
TITLE OF INVENTION: 58764, HUMAN TRANSFERASE FAMILY MEMBERS AND USES THEREFOR
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AND USES THEREFOR
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AND USES THEREFOR
CURRENT APPLICATION NUMBER: US/09/924,358
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/229,300
PRIOR APPLICATION NUMBER: US 60/229,300
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 191
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US-09-924-358-22
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Patent No. US20020107376A1
GENERAL INFORMATION:
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Best Local S
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Consensus amino acid
                                                                                                                                                                                                                                y Match 7.6%; Score 181; DB 10; Length 191;
Local Similarity 32.7%; Pred. No. 1e-08;
hes 65; Conservative 32; Mismatches 78; Indels 24;
                                                                                                                                                                                             259 REHIRESLGVRSEDLLFAIINSVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVGS 318
                                                                                                                           319 DVNAQT-KFETQLRDFVVKNTIHDRVHFVNKTLAVAP-----YLAAIDVLVQNSQGRG 370
                                                                                             61
                                                                                                                                                               2 REBIRKKLGIKEDKKIILFVGRLVPEKGIDLLIEAFKKLKKKPKLLKLN-PNLKLVIVGG
                          EGFGIVLLEAMACGLPVIATNCVGGIPEVVKDGETGLLVEPGQDPEA-LAEAIEKLLKDE 172
                                                     ECFGRITIEAMAFKLPVLGT-AAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHA 429
                                                                                              PYDSEDGEEEDELKKLAEKLGLEDNVIF----LGFVPDEDLPELYKSA-DVFVLPS--RY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-176-913-296
US-10-180-557-296
US-10-180-557-296
US-10-174-572-296
US-10-174-572-296
US-10-174-588-296
US-10-174-588-296
US-10-175-749-296
US-10-175-749-296
US-10-176-488-296
US-10-176-747-296
US-10-176-747-296
US-10-176-987-296
US-10-176-987-296
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US-10-176-992-296
US-10-176-993-296
US-10-173-695-296
US-10-173-765-296
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Database

Minimum DB Maximum DB

Scoring table: Perfect score: Sequence: OM protein -

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Result No.

Score

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CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: EP98202465.5
PRIOR FILING DATE: 1998-07-22
PRIOR APPLICATION NUMBER: EP98202467.1
PRIOR APPLICATION NUMBER: EP98202467.1
PRIOR FILING DATE: 1998-07-22
INUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 385
TYPE: PRT
TYPE: PRT
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US-09-924-358-25
; Sequence 25, Applic
; Patent No. US20020:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Consensus amino acid US-09-924-358-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/09767041 Patent No. US20020055168A1 GENERAL INFORMATION:
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: McBeth, Kyle
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226, AND
TITLE OF INVENTION: 58764,
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 38155-20034.00
CURRENT APPLICATION NUMBER: US/09/924,358
CURRENT FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-09-01
RNINBER OF SEQ ID NOS: 52
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Best Local Similarity
Matches 47; Conserv
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SEQ ID NO 25
LENGTH: 144
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TITLE OF INVENTION: STREP
FILE REFERENCE: 2183-4726
                  FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: CPS2G
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ORGANISM: Artificial Sequence
FEATURE:
TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 FETQLRDFVVKNTIHDRVHF---VNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGLPVIATTTDGGGCEEIIEDGENGLLVEPNNSDVEELAEALEKLLENEELRKKMMGKNA 121
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520020107376A1
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                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 3890
LENGTH: 387
TYPE: PRT
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                ; ORGANISM: Corynebacterium glutamicum US-09-738-626-3890
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US-09-738-626-3890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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179 LPKILWWIHEMRGH------YFKVEYVKHLPFVAGAMIDSHT---TAEYWNSRTSDR 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 SIEROKEHF 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 GKPVVGYRHGGVCEMVKEGVNGFL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 IDEEALVIGMVGRVNAWKGOGDFLEAVAPILE-----QNPKAIAFIAGSAFEGEEWRV 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 KIVTV---SQAVANHIKQSPHIKDDQISVIYNGVDNKVFYQSD---ARSV----RERFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 LVILNT--AVAGKWLDPVLKDHVPKVLPKILWWIHEMRGHYFKVEYVK-HLPFVAGAMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 LRHVGSQVVWITNQ--RSQETN-----DVTYSLEHRMLNHGVQVLPARGQEAVDIALKAD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 GYGRVKEMF 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 VELEKKISQLKVSSQVRRMDYYANTT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 LREVGAQVEVINYPILRRKYFNPKGIFDYFISYHH----YSKQI----AQYAIE--NKVD
                                                                                                          h 6.3%; Score 150; DB 9;
Similarity 24.4%; Pred. No. 2.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 6.8%;
Similarity 24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKEDA, MASATO
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIROSHI
                                                                43; Mismatches 124; Indels 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Mismatches 145; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 162.5; DB : Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VTPNSPLNLSKVILQLSENINLRKKIGNN 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ELYNMFDIFVLPST-NPDPLPTVVLKAMAC
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                                                                                                                                Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 385;
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US-09-767-041-18

Gaps

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Sequence 5, Application US/09924358

Patent No. US20020107376A1

GENERAL INFORMATION:
APPLICANT: Millemium Pharmaceuticals, Inc.
APPLICANT: Millemium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 58764,
TITLE OF INVENTION: 58764,
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AND USES THEREFOR
FILE REFERENCE: 38155-20034.00
CURRENT APPLICATION NUMBER: US/09/924,358
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/229,300
PRIOR APPLICATION NUMBER: US 60/229,300
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FASTSEQ for Windows Version 4.0

1 ENGTH: 416
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US-09-924-358-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 VSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVGSDVNAQTKFETQLRDFVVK----
                                                                                                                                                                                                                             125
337 NTIHDRVHFV---NKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAG 393
                                            233 RYERKKNLTLALEALVOLRGRLTSQDWE--RVHLIVAGGYDERVLENVEHYQELKKMVQQ 290
                                                                                                                                    174 LVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKL-DDLVPKGKKFLLLSIN
                                                                                                                                                                                228 KIQMPQTYVVHLGNSKELMEVAED-----NVAR--RVLREHIRESLGVRSEDLLFAIIN 279
                                                                                                                                                                                                                                                                     181 -----KILWWIH-----EMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRL 227
                                                                                                                                                                                                                                                                                                                                                                 138 VLPAR------GQEAVDIALKADLVILNTAV---AGKWLDPVLKDHVPKVLP-- 180
                                                                                                                                                                                                                                                                                                                     65 ELPVRCAGDWLPRGLGWGGRGAAVCAYVRMVFLALYVLFLADEEFDVVVVCDQVSACIPVF 124
                                                                                                                                                                                                                                                                                                                                                                                                              17 VLFLHPDLGVGGAERLVLDAALALQARGCSVKIWTAH-----YDPGHCFAES--R
                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 VLLVSHELSLSGGPLLLMELAFILRHVGSQV-VWITNQRSQETNDVTYSLEHRMLNHGVQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVDAVTSGEGGFF--ADDDSVESWVSKIDLLVSDPKLRDRMGRAGRQFVSARFNRDDVAA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAE 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQVTITGWIDFPEEP-----LAAVDVLLHPTQREG--LGMSLLEAQAMGVPVLTNAVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INKDKGGDLL-----AALTKHEAFTRLRLHLLIIGE-----LEDDDLREAFIKLVNE
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                                                                                       SVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVG----SDVNAQTKFETQLRDFVVK 336
                                                                                                                                                                                                                             RLARRRKKILFYCHFPDLLLTKRDSFLKRLYRAPIDW-----IEEYTTG------MADCI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.6%; Score 134.5; DB 10; Length 416; 21.7%; Pred. No. 0.00062; rative 61; Mismatches 193; Indels 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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US-09-738-626-4738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 409
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4738
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PELICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 4738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4738, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.6%;
Best Local Similarity 23.7%;
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405
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                             347
                                                                                                                                                                  346
                                                                                                                                                                                                            242
                                                                                                                                                                                                                                                           292
                                                                                                                                                                                                                                                                                                   191 LNGIDTELWQPRPTFDDAEDSVLR------SLGVDPORPIVAFVGRITRQKGVEHLI 241
                                                                                                                                                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                                                                                                                                             140 REQLGGGYDVSSWSEKNAMEYADAVIAVSARMKDSILAA------YPRIEPDNVRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                          186 IHEMRGHY-----FKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLKIQMPQTYVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 NHGVQVLPARGQEAVDIALKADLVILNTAVAGKWLDPVLKDH-VPKVL-----PKILWW 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 NPAIKTL-STGLRMAEAANNVDVVHSHTWYAGLGGHLAARLHGIPHVATAHSLEPDRPWK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
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TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQL 407
                                                                                                                                                                                                                                                                                                                                                   HLGNSKEL-----MEVAEDNVARRVLREHIRESLGVRSEDLLFAIINSVSRGKGQDLFL 291
                                ALVHYDENDVETFERDIAEAVNKMVADRETAAKFGLAGRERAINDFSWATIAQQTIDVYK 406
                                                                          LLHPAGKEGVAPLAKNIV----RLASHAEQRVSMGEKGYGRVKEMFMEHHMAERIAAVLK 461
                                                                                                                                                                  VNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTG 405
                                                                                                                                                                                                              KAAALFDESVQLVLCAGAPDTPEIAARTTALVEELQAKREGIFWVQDMLGKDKIQE---- 297
                                                                                                                                                                                                                                                      QA---FYQALQLIQHEKL-KVPRIHAVVVGSDVNAQTKFE--TQLRDFVVKNTIHDRVHF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAYASHI, MIKIRO
OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 133.5; DB 9 Pred. No. 0.00075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 160;

    IYEPLGIVNLEAMACNTAVVASDVGGIPEVVVDGTTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TETEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IXEDA, MASATO
APPLICANT: IXEDA, MASATO
APPLICANT: IXEDA, MASATO
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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US-09-738-626-3951
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Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT: MIZOGUCHI, HIROS!
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                                                                                                                                        351 AVAPYLAAIDYLYQNSQGRGECFGRITIEAMAFKLPYLGTAAGGTTEIVLDGSTGLLHPA 410
                                                                                                                                                                                           245 VAALFDRDPDRNLRV-----IICGGPSGPNATPDT-YRHMAEELGVEKRIRFLDPRPPSE 298
                                                                                                                                                                                                                                        294 FYQALQLIQHEKLKVPRIHAVVVGSDVNAQTKFETQLRDFVVKNTIHDRVHFVN---KTL 350
        353
                                                411 GKEGVAP--LAKNIVRLASHAEQRVSMGE 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                      174 HVPKVLPKILWWIHEMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLKIQMPQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 NS-YRDDSDTPESEARRICE------QOLVD---NADVLAVNTQEE------ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 NQRSQETNDVTYSLEHRMLNHGVQVLPARGQEAVDIALKADLVILNTAVAGKWLDPVLKD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 AAFTGGMLSFTRREKVTYDLIHSHYWLSG-----QVGWLLRDLWRIPLIHTAHTLAAVK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 AVASGSPLGFMRSKLVL--LVSHELSLSGGPLLLMELAFLLR------HVGSQVVWIT 113
                                                                                                                                                                                                                                                                                        -----GADVELYSPGNDRATERSRRE----LGIPLHTKVVAFVGRLQPFKGPQVLIKA 244
                                                                                                                                                                                                                                                                                                                                                                                         -----DADPDRISVVSP- 195
-VDGHSPHAWADALATLLDDDETRIRMGE 380
                                                                                          LVAVYRAADIVAVPSF----NESFGLVAMEAQASGTPVIAARVGGLPIAVAEGETGLL---
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ANDO, SEIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Mismatches 151; Indels 109;
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US-09-738-626-5896

RESULT 8

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APPLICATI: Neyers, Rachel A.

FITTLE OF INVENTION: 33877 AND 47179, NOVEL HUMAN

FITTLE OF INVENTION: GLYCOSYLTRANSFERASE FAMILY MEMBERS AND USES THEREOF

FILE REFERENCE: 10448-033001

CURRENT APPLICATION NUMBER: US/09/815,028

CURRENT FILING DATE: 2001-03-22

PRIOR APPLICATION OF SECTION OF SECT
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR PPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
VINMBER OF SEQ ID NOS: 7059
SOPITWARE: PATENTIN NOS: 7059
SOPITWARE: PATENTIN NOS: 7059
SOPITWARE: PATENTIN NOS: 7059
SOPITWARE: PATENTIN NOS: 7059
SOPITWARE: PATENTIN Ver. 3.0
TYPE: PRI
ORGANISM: COTYDEDACTETIUM Glutamicum
US-09-738-626-5896
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US-09-815-028-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 ELLDDPIRRAAMGAAGRAHVEAEWSWEIMGERLTNILQ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 RLASHAEQRVSMGEKGYGRVKEMFMEHHMAERIAAVLK 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 RESLGVRSEDLLFAIINSVSRGKGODLFLQAFYQALQLIQHEKLKVPRIHAVVVGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ECFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEG--VAPLAKNIV 423
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TATEISHI, NAOKO
SENOH, AKIHIRO
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OZAKI, AKIO
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OCHIAI, KEIKO
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ANDO, SEIKO
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PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2002-01-14

PRIOR PILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 166

SOFTWARE: Patentin version 3.1

SEQ ID NO 107

LENGTH: 371

TYPEP: """
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; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-870-759-107
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US-09-870-759-107
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APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 870759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 107, Application US/09870759 Patent No. US20020177551A1
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Best Local Similarity
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CURRENT FILING DATE: 2002-01-14
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                 344
                                                         436
                                                                                                                                                                                                                                                                                                   259 REHIRESLGVRSEDLLFAIINSVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVGS 318
                                                                                                                                                                                                                                                                                                                                             50;
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                                                                                                                                                                               236 D--KPRKFEA----LAEKLGVRSNVHFFSGRNDVSELMAAADLLLHPAY--QEAAGIVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 VLLVSHELSLSGGPLLLMELAFLLRHVGSQV-VWITNQRS----QETNDVTYSLEHRMLN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; Conservative
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Similarity 24.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVTGFLCEPDPVHFSEAIEKFIREPS---LKATMGLAGRAKVKEKFSPEAFTEQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVFKKTFKTLSHIDPDVLYPSLNVTSFDSVVPEKL-DDLVPKGKKFLLLSINRYERKKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVHLGNSKELMEVAED-----NVAR--RVLREHIRESLGVRSEDLLFAIINSVSRGKGQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILFYCHFPDLLLTKRDSFLKRLYRAPIDW-----IEEYTTG-----MADCILVNSQFTA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILWWIH-----EMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLKIQMPQTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGL----GWGGHGAAVCAYVRMVFLALYVLFLADEEFDVVVVCDQVSACIPVFRLARRKK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLRSFSDKQKISLLHSCTCVLYTPS---NEHPGIVPLEAMYMQCPVIAVNSGGPLESIDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLALEALVOLRGRLTSQDWE--RVHLIMAGGYDERVLENVEHYQELKQMVQQSDLGQYVT
                 AENARHYADTQDLY---SLPEKAADII 367
                                                                                                                                       EAMAFKLPVLGTAAGGTTEIVLDGSTG--LLHPAGKEGVAPLAKNIVRLA-SHAEQRVSM 435
                                                                                                                                                                                                                   DVNAQTKFETQLRDFVVKNTIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITI 378
                                                                                                                                                                                                                                                             REIYROKNGIKEQQNLLLQVGSDFGRKGVDRSIEALASLPESLRHNTL-----LFVVGQ 235
                                                         GE--KGYGRVKEMFMEHHMAERIAAVL 460
                                                                                               EAITAGLPVLTTAVCGYAHYIADANCGTVIAEPFSQEQL----NEVLRKALTQSPLRMAW 343
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.3%; Score 126.5; DB 10; Length 21.2%; Pred. No. 0.0034; ative 66; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                             40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Score 118; DB 9; Length 371; Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOR TREATMENT OF NEOPLASTIC DISEASE
                                                                                                                                                                                                                                                                                                                                             91;
                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Synechocystis sp. US-10-217-700-14
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US-10-217-700-14
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US-10-174-590-296
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TITLE OF INVENTION: TRANSCENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/10/217,700
CURRENT FILING DATE: 2002-08-12
EARLIER APPLICATION NUMBER: 09/394,272
EARLIER FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 720
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Publication No. US200
GENERAL INFORMATION:
                                                                                                                                                                                                                                           Sequence 296, Application US/10174590 Publication No. US20030008352A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.7%; Score 113; DB Best Local Similarity 21.7%; Pred. No. 0.14;
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APPLICANT:
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                                                                                                                                                                               APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
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                                                                               APPLICANT:
                                       APPLICANT:
                                                                APPLICANT:
CANT: Watanabe, Colin K.
CANT: Wood, William I.
CANT: Zhang, Zemin
OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378
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                                                                                                                                                                                                                                                                                                                                                                                                                                      448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 IHDRVHFVNKTLAVAPYLAAIDVLVQNSQG-----RGECFGRITIEAMAFKLPVLGTAA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 SRPDPRKNIHKLIAAYGQSPQLQAQANLVIVAGNRDDITDLDQGPREVLTDLLLTIDRYD 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 AEQYAQYDYYQPDQMLVIPPGTD--LEKFYPPKGNEWETPIVQELQRFLRHPRKPIILAL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 GHSLGRSKRTRLLLSGIKADEIESRYNMARRINAE--EETLGSAAR-----VITSTHQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 VH-LGNSKE----LMEVAED-----NVARRVLREHIRESLGVRSEDLLFAIINSVSR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 VLPKILW-WIHEMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLKIQMPQTYV
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                                                                                               Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGPVDIIKNCONGYLINPLDE----VDIADKLLKVLNDKOOWOFLSESGLEGVKRHYSWPS 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTEIVLDGSTG-LLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMF----
                                                                                                                                                                                                                                                                                                                                                                                                                                 -MEHHMAERIAAVLK--DVLRKS
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lo. US20030070191A1
                                                                                  Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                      467
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377

308 201 283

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TILE REFERENCE: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/10/176,758

CURRENT FILING DATE: 2002-06-21

Prior Application removed - See File Wrapper or Daily Region 10 NOS: 612

SEQ ID NO 296

LENGTON 296
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; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-19
; Prior application removed - See File Wrapper
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 296
; SEQ ID NO 296
; SEQ ID NO 323
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                                                                                                                                                         ; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-758-296
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US-10-176-758-296
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                                                                        Query Match 4.6%; Score 111; DB 9; Length 323; Best Local Similarity 22.6%; Pred. No. 0.062; Matches 67; Conservative 46; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 296, Application US/10176758 Publication No. US20030008353A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 67; Conserv
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                                181 KILWWIH-----EMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLKIQMPQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 QDLFLQAFYQALQLIQHEKLKVFRIHAVVVG---SDVNAQTKFETQLRDFVVKNTIHDRV
39 KILFYCHFPDLLLTKRDSFLKRLYRAPIDW-----IEEYTTG-----MADCILVNSQFT
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Godowski, Paul
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    See File Wrapper or

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    score 111; DB 9; Length 323;
    Pred. No. 0.062;
    Mismatches 143; Indels

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RESULT 14
US-10-175-737-296
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; GENERAL INFORMATION;
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US-10-175-737-296
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Best Local S
Matches 67
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 296
LENGTH: 323
TYPE: PRT
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
                                           401
                                                                                                            344 HFV---NKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTTEIVL
                                                                                                                                                   147 LTLALEALVOLRGRLTSODWE--RVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYV
262 HSVTGFLCEPDPVHFSEAIEKFIREPS---LKATMGLAGRARVKEKFSPEAFTEQL
                                                                         205 TFLRSFSDKQKISLLHSCTCVLYTPS---NEHFGIVPLEAMYMQCPVIAVNSGGPLESID
                                                                                                                                                                                      287 QDLFLQAFYQALQLIQHEKLKVPRIHAVVVG----SDVNAQTKFETQLRDFVVKNTIHDRV
                                                                                                                                                                                                                                                                235 YVVHLGNSKELMEVAED-----NVAR--RVLREHIRESLGVRSEDLLFAIINSVSRGKG
                                                                                                                                                                                                                                                                                                                                          181 KILWWIH-----EMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLKIQMPQT
                                                                                                                                                                                                                             88 AAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKL-DDLVPKGKKFLLLSINRYERKKN
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67; Conserv
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                                                                                                                                                                                                                                                                                                     39 KILFYCHFPDLLLTKRDSFLKRLYRAPIDW-----IEEYTTG-----MADCILVNSQFT
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                                DGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAERI 456
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Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 143;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C7
CURRENT APPLICATION UMBER: US/10/173,706
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 296
LENGTH: 323
TYPE: PRT
ORGANISM: Homo Sapien
US-10-173-706-296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.6%; Score 111; DB 9; Length 323; Best Local Similarity 22.6%; Pred. No. 0.062; Matches 67; Conservative 46; Mismatches 143; Indels 40; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KILWWIH-----EMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLKIQMPQT 234
262 HSVTGFLCEPDPVHFSEAIEKFIREPS---LKATMGLAGRARVKEKFSPEAFTEQL 314
                                               401 DGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAERI 456
                                                                                                 205 TFLRSPSDKQKISLLHSCTCVLYTPS---NEHFGIVPLEAMYMQCPVIAVNSGGPLESID 261
                                                                                                                           344 HFV---NKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLFVLGTAAGGTTEIVL 400
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                                                                                                                                                                                                                                                                                                                                          235 YVVHLGNSKELMEVAED-----NVAR--RVLREHIRESLGVRSEDLLFAIINSVSRGKG 286
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Godowski, Paul J.
Gurney, Austin L.
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Search completed: June 30, 2003, 16:35:04 Job time : 55 secs

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| | lipopolysaccharide | AD0973 | | ۳. | | 149 | 19 |
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| | 430 | 379 | 364 | 417 | 230 | 390 | 385 | 422 | 376 | 344. | 316 | 427 | 429 | 380 | 354 | 412 |
| | N | N | N | N | N | _ | N | N | N | N | N | N | N | N | N | N |
| | AI2455 | S77338 | H75466 | AB2359 | G81870 | A75059 | D97911 | AH2352 | A82676 | C81152 | F70441 | B95936 | AB2456 | B97275 | AG3315 | T35514 |
| | glycosyltransferas | LPS glycosyltranst | lipopolysaccharide | hypothetical prote | probable glycosyl | probable hexosyltr | hypothetical prote | hypothetical prote | conserved hypothet | LPS biosynthesis p | capsular polysacch | probable glycosylt | glycosyltransferas | glycosyltransieras | Lipopolysaccharide | probable glycosyl |

ALIGNMENTS

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|---|---|---|---|--|--|--|--|
| Qy 389 GTAAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFM 448 :: : : : : : : | Qy 329 QLRDFVVKNTIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVL 388 : : : : : | Qy 269 RSEDLLFAIINSVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVGSDVNAQTKFET 328 | Qy 209 MIDSHTTAEYWNSRTSDRLKIQMPQTYVVHLGNSKELMEVAEDNVARRVLREHIRESLGV 268 | Qy 149 IALKADLVILNTAVAGKWLDPVLKDHVPKVLPKILWWIHEMRGHYFKVEYVKHLPFVAGA 208 :: | Qy 89 SGGPLLLMELAFLLRHVGSQVVWITNQRSQETNDVTYSLEHRMLNHGVQVLPARGQEAVD 148 | Query Match 61.7%; Score 1478; DB 2; Length 402; Best Local Similarity 74.5%; Pred. No. 9.6e-102; Matches 283; Conservative 53; Mismatches 44; Indels 0; Gaps 0; | RESULT 1 G96784 Gypothetical protein FIB16.5 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: G96784 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conm, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, J.R.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, J.R.; M.; W., D.; Yu, G.; Fraser, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II, A.; M.; W., D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Genetics: preliminary A;Status: preliminary A;Genetics: F1B16.5 A;Genetics: A;Gene |

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318

GTAAGGTMEIVVNGTTGLLHSAGKEGVIPLAKNIVKLATQVELRLRMGKNGYERVKEMFL

377

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hypothetical protein F6F9.24 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: A86330
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Asher, N.F.; Hughes, B.; Huizar, L.
Mature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Aluthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86130
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Rosesion: A86330
A;Residues: 1-458 <570>
A;Cross-teferences: GB:AB8005172; NID:g10086496; PIDN:AAG12556.1; GSPDB:GN00141
C;Genetics:
C;Genetics:
A;Map position: 1
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Similarity 62.8%;
                                                                                                                                                                                                                                                                         LAVAPYLAAIDVLVQNSQGRGBCFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTGLLHP
                                                                                                    HSRS 473
                                                                                                                                            TGKDGVLPLAKNIVKLATNVKMRNTMGKKGYERVKEMFLEHHMSHRIASVLREVLQHAKI
                                                                                                                                                                                 AGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAERIAAVLKDVLRKSQE 469
                                                                                                                                                                                                                                      MKVAPYLAAIDVLVQNSQARGECFGRITIEAMAFKLPVLGTAAGGTMEIVVNRTTGLLHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DPAALNTAVASGS--PLGFWRSKLVLLVSHELSLSGGPLLLMELAFLLRHVGSQVV 110
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Pred. No. 3.8e-101;
S5; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 458;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96564
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A
Chin, C.W.; Chung, M.K.; Conn, L.;
Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewa
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Mar
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzbergy, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96564
hypothetical protein AGR_L_2541 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 C;Accession: D98299
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A; Residues: 1-670 <S
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Matches 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 ATYGKILGPFGSLEDKVLEWSPHRRSGTCDRKSD------FKRLVWSRRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 ARGQEAVDIALKADLVILNTAVAGKWLDPVLKDHVPKVLPKILWWIHEMRGHYFK-----
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                                                                                                                                                                                 GRKMVEKMYMKQHMYKRFVDVLVKCMR
                                                                                                                                                                                                                              GYGRVKEMFMEHHMAERIAAVLKDVLR 465
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                                                                                                                                                                                                                                                                                                                   EAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEK
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29.2%; Pred. No. 9.7e-28;
7ative 77; Mismatches 173;
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Maiti, R.; Marziali,
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| A;Gene: Atu3560 A;Map position: linear chromosome 8.6%; Score 207; DB 2; Length 382; Query Match Best Local Similarity 27.5%; Pred. No. 1.1e-07; Matches 68; Conservative 46; Mismatches 109; Indels 24; Gaps 7; Matches 68; Conservative 46; Mismatches 109; Indels 27; Oy 20 NSRTSDRLKIQMOTYVVHLGNSKELMEVABDNVARRVLREHIRESLGVRSEDLLF 275 | RESULT 5 AP2994 AP2994 C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: IJan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AF2994 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W. A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Accession: AF2994 A;Accession: AF2994 A;Status: preliminary A;Residues: 1-382 <kur> A;Residues: 1-382 <kur> A;Cross-references: GB:AE008689; PIDN:AAL44372.1; PID:g17741967; GSPDB:GN00187 A;Experimental source: strain C58 (Dupont) C;Genetics:</kur></kur> | | R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2232-3228, 2001 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194 A;Accession: D98289 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-382 KUR> A;Cross-references: GB:AE007870; PIDN:AAK89838.1; PID:g15159774; GSPDB:GN00170 C;Genetics: A;Gene: AGR L 2541 A;Map position: linear chromosome |
|---|---|--|---|
| OY | 87 SISG 50 SPG 50 SPG 146 AVDI :::: 100 SIKL 205 VAGR :: 151 LWRC 253 VARR 251 VELK 307 KUPR 307 KUPR | RESULT 6 G71096 G71096 hypothetical protein pH1035 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii R;Kawarabayasi, Y; Sawada, M.; Horikawa, Y; Hino, Y; Yamazaki, J; Yamamoto, S; Sekine M.; Ohiku, Y; Yamazaki, J; Yamazaki, J; Yamamoto, S; Sekine M.; Ohiku, Y; Yamazaki, J; Yamazaki, J; Yamamoto, S; Sekine M.; Ohiku, Y; Yamazaki, J; Yamazaki, J; Yamazaki, J; Sekine M.; Ohiku, Y; Yamazaki, J; Yamazaki, J; Yamazaki, J; Yamazaki, J; Sekine M.; Ohiku, Y; Yamazaki, J; Yamazaki, J; Yamazaki, J; Yamazaki, J; Sekine M.; Ohiku, Y; Yamazaki, J; | Db 208 GLEGRISEWKGOHVELDAL-AAMEGVQAVIVGGALEGQEAYEARIREQAS 256 Qy 336 KWITHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECEGRITIBAMAFKLPVLGTAAGGT 395 |

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R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-ther A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Gene: PH1844
C;Superfamily: probable hexosyltransferase ytxN
                                                                                                  A;Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA30965.1; PID:g3258282 A;Bxperimental source: strain OT3 A;Note: this accession replaces an interim accession for a sequence replaced C;Genetics:
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A; Residues: 1-381 < KAW>
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A;Residues: 1-388 <ARN)
A;Residues: 1-388 <ARN)
A;Residues: 1-388 <ARN)
A;Cross-references: GB:AE001736; GB:AE000512; NID:g4981138; PIDN:AAD35706.1;
A;Experimental source: strain MSB8
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A;Accession: E72354
A;Status: preliminary
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A;Title: Evidence for lateral gene transfer between Archaea and **Deference number: A72200; MUID:99287316; PMID:10360571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVLKOVLRKSQEHSR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLEEKVKFFGVRSDVPELLSQADIFVLSSDYEG--FGLVVAEAWAAGLPVIATAIGGIPE
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Conservative 58;
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23.5%; Pred. No. 3e-06;
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C; Keywords: glycosyltransferase; hexosyltransferase
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                                     LASHAEQRVSMGEKGYGRVKEMFMEHHMAERIAAVLKDVLRK
                                                                              IŚ---SEAFGIVILEAMASGVPIIATDVGGIPEVIKENSAGLLVPPGNE--LKLREAIEK 338
                                                                                                                   NSQGRGECFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVR 424
                                                                                                                                                                                                    RIHAVVVGSD-----VNAQTKFETQLRDFVVKNTIHDRVHFVNKTLAVAPYLAAIDVLVQ 364
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LLKNEELRKWYGNNGRRSVEEKYSWNKIVVKIERIYNEVLQE
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                                                                                                                                                                                                                                                                                  ----REHIRESLGVRSEDLLFAIINSVSRGKGQDLFLQAFYQALQLIQHEKLKVP 309
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A;Cross-references: GB:AE003927; GB:AE003849; NID:g9105783; PIDN:AAF83689:1; GSPDB:GN001; A;Experimental source: strain 9a5c
R.Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Netc, B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A.Authbors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
Chado, M.A.; Madeira, A.M. B.N.; Madeira, H.M.F.; Marino, C.L.; Marquees, M.V.; Mattins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.,
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasakı
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za
A,Reference number: AS9328
A,Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-370 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: E82751

R;anonymous, The Xylella fastidiosa Consortium of the Organization for NN Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below A;Accession: E82751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipopolysaccharide biosynthesis protein XF0879 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa (c;Species: Xylella fastidiosa (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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h 7.2%; Similarity 25.0%; 79; Conservative 4

48;

Score 172.5; DB 2 Pred. No. 3.7e-05; 48; Mismatches 136

Indels Length 370;

53;

Gaps

12;

DB 2;

| Similarity 24.6%; Pred. No. 0.0001; 5; Conservative 58; Mismatches 153; 6; Conservative 58; Mismatches 153; 7; Conservative 58; Mismatches 153; 8; Mismatches 153; 8; Mismatches 153; 9; Mismatches 153; 1 | | | OY 178 VLPKIL |
|--|---|--|---|
| Oy 391 AAGGTTE VLOSVIGLHAPGK | 104 HVGSQVYWITNQRSQETNDVTYSLEHRMLNHIGVOVLPARGQEAVDIALKADDVI | estical protices: Nostoco sp: 14-Dec 20 ssion: AD2-20 ssio | Qy 307 KVPRIHAVVVGSDVNAQTKFETQLRDEVVKNTIH |

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R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixin A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: H95920
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-416 <KUR>
                                                                                                                                             probable membrane-anchored glycosyltransferase protein SMb21053 C;Species: Sinorhizobium meilloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change C;Accession: H95920 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.;
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R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.

A;Aritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
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A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-405 <STO>
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                    390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 HGVQVLPAR----GQEAVDIALKADLVILNTAVAGKWLDPVLKDHVPKVLP------KI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
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97; Conserv
                                                                                                                                                                                                                                                                                                                                                    RIAAVLKDVLRKSQE 469
                                                                                                                                                                                                                                                                                                                                                                                   VETVKNGVTGYLCEPTPEDFSSAMA----RFIENPELANRMGAEARNHVVESFSVKTFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                       TEIVLDGSTG-LLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HFV-----NKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFLQAFYQALQLIQHEKLKVPRIHAVVVG-----SDVNAQTKFETQLRDFVVKNTIHDRV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEYCHEPDLLLAKHTTTLRRMYRKPIDFIEEQTTGMADMILVNSNFTASTF-ANTFKRLN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LWWIH-----EMRGHYFK-VEYVKHLPFVAGAMI--DSHTTAEYWNSRTSDRLK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YG-SFLPRHIFYRLHAVCAYLRCLFVALCVLLGWSSFDVVLADQVSVVVPLLKLKRSSKV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKMNIAIIHPDLGIGGAERLIVDAAVELASHGHKVHIFTSHHDKSRCFEETLSGIFQVTV 66
                                                                                                                                                                                                                                                                                                                    KLNOYLVDVVSSPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFITSCSTAERNELLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAVSAF----AILCKHKONLSDVTLTVAGKCGYDERLKENVEYLEELRSLAEKEGVSDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQMPQTYVVHLGNSKELMEVAEDNVARRVLREHIRESLGVRSEDLLFAIINSVSRGKGQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQGSRPAVLYPA-----
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                                                                                                                                                                                                                                                                                                                  404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 161; DB 2;
Pred. No. 0.0003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SCLCVLYTPTD---EHFGIVPLEAMAAYKPVIACNSGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                            30-Sep-2001
                                                                                                                                                                                                                [imported] -
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H64446
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                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
358 AIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                              Similarity
                                        ----IKDIDFNFKLIGDG---
                                                                        QLIQHEKLKVPRIHAVVVGSDVNAQTKFETQLRDFVVKNTIHDRVHFVNKTL-AVAPYLA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                        27.2%;
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A;Cross-references: GB:AL591985; PIDN:CAC49032.1; PIDig15140517; GSPDB:GN00167
A;Bxperimental source: strain 1021, megaplasmid pSymB
R;Gailbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.,
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; pMID:11474104
A;Contents: annotation
                                                                                                                                                                                                                                   354 PYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKE 413
                                                                                                                                                                                                                                                                                                                   250 LPVDFLTSLSSDPRVLDLKRFYDQWNRCRYQQHLDELMDRHRLRHRIRFLGNVSHKELVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 HIRESLGVRSED-----LLFAIINSVSRGKGODLFLQAFYQALQLIQHEKLKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFRPSEAGASGDARTGRVILF--VGRISPEKGLHTLVEAFSEVALRFPDVELRIAGPYSP 249
G--ELSQALITVLDDPARARGMGTEGRERAVALYSWEARAERLRSVYERVSR
                                                                           GVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAERIAAVLKDVLR 465
                                                                                                                                                            AYHDA-DIVVNPS--LSESFGISVVEGMACGIPVVGTRVGGMCESILDGHTGMLVEADAP
                                                                                                                                                                                                                                                                                                                                                                                                    -----PRIHAVVVGSDVNAQTKFETQLRDFVVKNTIHDRVHF---VNKTLAVA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 156; DB 2;
Pred. No. 0.00072;
1; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                        309
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A;Start codon: GTG
C;Superfamily: probable hexosyltransferase ytxN
C;Keywords: glycosyltransferase; hexosyltransfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable hexosyltransferase (EC 2.4.1.-) MJ178 [similarity] - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000 C;Accession: H64446 R;Bult, C.J.; Mitte, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A., Feon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 Science 273, 1058-1073, 1996 R;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:U67559; GB:L77117; NID:g1591798; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-351 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A64300; MUID:96337999;
A;Accession: H64446
                                                                     242 SKELMEVAEDNVARR--VLREHIRESLGVRSEDLLFAI-INSVSRGKGODLFLQAFYQAL
SKYIKNQLDENLKNRAIVIYNGVNKEILYNEGDYNFGLFVGAFVPQKGVDILIDA-----
                                                                                                                                                                           6.4%; Score 154.5;
27.2%; Pred. No. 0.0
                                                                                                                                                                                                                                                                         hexosyltransferase
                                                                                                                                              Mismatches
                                                                                                                                                                           ).00073;
                                                                                                                                          Indels
                                                                                                                                                                                                        Length
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                                                                                                                                      25;
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g1591805;
       200
                                                                        298
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--KLYKKIENFVVKNNLSHIELLGRKSFDEVASFMR

248

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probable lipopolysaccharide N-acetylglucosaminyltransferase (EC 2.4.1.56) - Salmonella typhimurium C;Species: Salmonella typhimurium C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 08-Oct-1999 C;Accession: C41317 R;MacLachlan, P.R.; Kadam, S.K.; Sanderson, K.E. J. Bacteriol. 173, 7151-7163, 1991 A;Title: Cloning, characterization, and DNA sequence of the rfalk region for lipopolysac A;Reference number: A41317; MUID:92041612; PMID:1657881 A;Accession: C41317
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A;Molecule type: DNA
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A;Cross-references: GB:M73826; NID:g154328; PIDN:AAA27207.1; PID:g454851
C;Keywords: glycosyltransferase; hexosyltransferase
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P46915 bacillus su
P26470 salmonella
P3642 staphylococ
P54138 mycobacteri
Q11152 mycobacteri
P25740 escherichia
Q04975 salmonella
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Q9h294 homo sapien
P04713 zea mays (m
Q95911 rhizobium m
P09842 hordeum vul
Q25981 methanobact
Q48453 klebsiella
Q15397 homo sapien
Q50612 mycobacteri
Q30272 mycobacteri
Q10190 phaseolus a
Q43114 sorghum bic
Q19508 haemophilus
P53451 fugu rubrip
Q00775 solanum tub
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- FUNCTION: ACTS AT TRANSFER OF MANNOSE GROUP TO A 3-DEOXY-D-MONO OCTULONIC ACID (KDO) VIA AN ALPHA-1,5 LINKAGE (BY SIMILARITY).

- PATHWAY: Lipopolysaccharide core biosynthesis.
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lipopolysaccharide core biosynthesis mannosyltransferase (EC 2.-.-).
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Lagares A., Hozbor D.F., Niehaus K., Pich Otero A.J.L
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region involved in lipopolysaccharide biosynthesis.";
J. Bacteriol. 183:1248-1258(2001).
                                                                                                                                           EMBL; AF193023; AAF06008.1; EMBL; AL591787; CAC46151.1;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
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                                         InterPro; IPR001296; Glycos_transf_1.
Pfam; PF00534; Glycos_transf_1; 1.
Lipopolysaccharide biosynthesis; Transferase; Glycosyltransferase;
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Best Local :
Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Erritz C., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizri A., Galleron N., Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
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P46915;
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STRAIN=168 / 60015;
MEDLINE=95400496; PubMed=7545510;
MEDLINE=95400496; PubMed=7545510;
Abe A., Kolde H., Kohno T., Watabe K.;
"A Bacillus subtilis spore coat polypeptide
"Microbiology 141:1433-1442(1995).
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41,
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillales; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 180.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9B436AB9DB82377A CRC64;
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RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medique C.,

RA Hee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,

RA Medina N., Mellado R.P., Mizuno M., Moetl D., Nakai S., Noback M.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Presecan E., Fujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Presecan E., Fujic P., Purnelle B., Roce B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sorokin A., Tacconi E., Takagi T., Takhashi H., Takemaru K.,

RA Sorokin A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,

Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

Van Tanakoshi A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

"The complete genome sequence of the Gram-positive bacterium Baciilus in the sequence of the gram-posi
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InterPro; IPRO01295; Glycos transf_1.
Pfam; PF00534; Glycos transf_1; 1.
Spornlation; Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 377 AA; 42912 MW; 1F978E1B79F9E660 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Assembly of the CotSA coat protein into spores requires CotS
Bacillus subtilis.";
FEMS Microbiol. Lett. 174:201-206(1999).
-i- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D31847; BAA06633.1; -. EMBL; AF008220; AAC00219.1; -. EMBL; Z99119; CAB15069.1; -.
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CHARACTERIZATION
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328
                                                                       415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHYFKVEYVKHLPFVAGAMIDS----HTTAEYWNSRTSDRLKIQMPQTYVVHLGNSKELM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGVQVLPARGQEAVDIALKA----DLVILNTAVAGKWLDPVLKDHVPKVLPKILWWIHEMR 190
PKQYAERINDLLSSSEKRERLGKYSRREAESNFGWQRVAENLLSV 372
                                                                       VAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAERIAAV
                                                                                                                                                             YTMSDVFVCSSQWQ-EPLARVHYEAMAAGLPIITSNRGGNPEVIEEGKNGYIIHDF-
                                                                                                                                                                                                                                         LAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTG-LLHPAGKEG
                                                                                                                                                                                                                                                                                                                                                                                                  KVPRIHAVVVGSDVNAQTKF--ETQLRDFVVKNTIH-----DRVHFVN--KTLAVAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPRWTNEGQRA-REEMRSELGLHGKKIVL-FVGRLSKVKGPHILLQALPDIIE--EH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVAEDNVARRVLREHIRESLGVRSEDLLFAIINSVSRGKGQDLFLQAFYQALQLIQHEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYVHLDEDRYEEAVGAELKKSRFDLV--HVCNRPSWV-PKLKKQAPDAV--FILSVHNEM
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                                                                                                                                                                                                                                                                                                                      ----KWFGDNELNNYV--KHLHTLGAMQKDHVTFIQFVKPKDIPRL
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Pred. No. 1.1e-05;
8; Mismatches 153;
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01-AUG-1992
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MEDLINE-21534948; PubMed:11677609;

McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Lipopolysaccharide core biosynthesis.
-!- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
-!- SIMILARITY: SOME, WITH B.SUBTILIS YTXN.
-!- SIMILARITY: SHOWS VERY LITTLE SIMILARITY TO E.COLI RFAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipopolysaccharide 1,2-N-acetylglucosaminetransferase RFAK OR WAAK OR STM3714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maclachlan P.R., Kadam S.K., Sanderson K.E.; "Cloning, characterization, and DNA sequence of the rfalk region lipopolysaccharide synthesis in Salmonella typhimurium LT2."; J. Bacteriol. 173:7151-7163(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=LT2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma
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                                                                                                                                                                                      InterPro; IPR001296; Glycos transf 1.
Pfam; PF00534; Glycos_transf 1; 1.
Lipopolysaccharide biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                       StyGene; SG10339; rfaK.
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EMBL; AE008872; AAL22573.1; -.
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                                                                                                                                                                                                                                                        PIR; C41317; C41317
                                 133
                                                                168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   popolysaccharide.
                                                                                            Similarity 23.74; Conservative
 KIQMPQTYVVHLGNSKELMEVAEDNVARRVLREHIRESLGVRSEDLLFAIINSVSRGKGQ 287
                                 EPELPDNDAKII-------VPSQFLKAFYEERLPAAAVSIVPNGFCAETYKRNPQDNL
                                                                                                                                                                        proteome.
                                                              DPVLKDHVPKVLPKILWWIHEMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRL
                                                                                                                                                            381 AA; 43152 MW; F60F37FF175372C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 23, Created)
(Rel. 23, Last sequence update)
(Rel. 41, Last annotation updat
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                                                                                                             6.4%;
                                                                                              40;
                                                                                            Score 153; DB
Pred. No. 0.00
40; Mismatches
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                                                                                                               DB 1;
00012;
                                                                                               110; Indels
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                                                                                                                         Length 381;
                                                                                                                                                            CRC64;
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01-FEB-1995
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAPM STAAU
P39862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.";
J. Bacteriol. 176:7005-7016(1994)
-!- FUNCTION: REQUIRED FOR THE BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U10927; AAA64652.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin W.S., Cunneen T., Lee C.Y.; "Sequence analysis and molecular characterization of genes required for the biosynthesis of type 1 capsular polysaccharide in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95050273; PubMed=7961465;
Lin W.S., Cunneen T., Lee C.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus. Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capsular polysaccharide (EC 2.-.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interPro;
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      407
                                                                                                                        347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro; IPR001296; Glycos_transf_1.
PF00534; Glycos_transf_1; 1.
                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                           QLIQHEKLKVPR---IHAVVVGSDVNAQTK-----FETQLRDFVVKNTIHDRVHFV
   LHPAGKEGVAPLAKNI VRLASHAEQRVSMGEKGYGRVKEMFMEHHMAERI AAVLKDVLRK
                                                                                                                  NKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTGL
                                                                                                                                                                                ELIQSFKIIVSKGYNVKLLVIGS---LETENSIDESDYLFLTQNPNVVLIKHVSDPISFY
                                                          NN------MNVFVFPTHREG--FGNVSIEAQALEVPVITTNVTGAIDTVVNGETGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSWENVAQRFEEQMKN 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASKKGGISEFVLDGITGYHLAEPMSSDSII----NDINRALADKERHQIAEKAKSLVFSK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAAGGTTEIVLDGSTG--LLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEM
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5 (Rel. 31,
1 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                   5.6%;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                  Score 134.5; DB
Pred. No. 0.0035;
8; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                           0264E8376CD1A9EF CRC64;
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glycosyl
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                                                                                                                                                                                                                                                                                                  69;
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                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                      29;
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                                                                                                                                                                                270
                                                                                                                  406
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-Y486 MYCLE
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-P54138; Q9CB50;
01-OCT-1996 (Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Feltwell T., Fraser A., Hamlin N.,
Bavies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Smith D.R., Robison K.; Submitted (MAR-1994) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation updat
Hypothetical protein ML2443.
ML2443 OR U2168F OR B2168_C2_201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001296; Glycos transf_1.
Pfam; PF00534; Glycos transf_1; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 428 AA; 45291 MW; A14F9F0187E3587C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-i- SIMILARITY: TO M.TUBERCULOSIS RV0486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Squares S., Stevens K., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium leprae.
Bacteria, Actinobacteria, Actinobacteria (class), Actinobacteridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leproma; ML2443; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Corynebacterineae;
                                                                                                                                                                             114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U00018; AAA17228.1; ALT_INIT.
AL583925; CAC31960.1; -.
                                                                                                                  57
                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                  54
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
-IVHSH-----YWLSGQVGWLARDRWA--VPLVHTA----HTLAAVKNAALADGDA
                                                    PVLKDHVPKVLPKILWWIHEMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLK
                                                                                                                                                                         NORSOETNDVTYSLEHRMLNHGVQVLPARGQEAVDI-----ALKADLVILNTAVAGKWLD
                                                                                                                                                                                                                                    GIGDAGGMNVYVLQ-SALHLARRGIEVEIFTRATASADP-------PIVWVA
                                                                                                                                                                                                                                                                                                  GRGDPAALNTAVASGSPLGFMRSKLVLLVSHELSLSGGPLLLMELAFLLRHVGSQVVWIT 113
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris [A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamiln N., Holroyd S., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

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01-OCT-1996 (Rel. 34, Last sequence up
15-UNN-2002 (Rel. 41, Last annotation
Hypothetical protein Rv0486.
RV0486 OR MT0504 OR MTCY20G9.12.
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Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
Submitted (ApR-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO M.LEPRAE ML2443.
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Palson R., Gwinn M.L., Haft D., Hickey E.,
Peterson J.F., DeBoy R., Dodson R., Gwinn M.L., Ermolaeva M.D., Salzberg
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H.; Gill J., Mikula
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                                                                                                  equires a license agreement (S email to license@isb-sib.ch).
       CAB00947.1; -.
1; AAK44727.1;
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Tuberculist; R0448; -.
InterPro; IPR001296; Glycos transf_1.
Pfam; PF00534; Glycos transf_1; 1.
Pfam; PF00534; Glycos transf_1; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 480 AA; 50541 MW; 2134755E894A9CCF
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G.
"Analysis of the Escherichia coli genome. V. DNA
region from 76.0 to 81.5 minutes.";
                                                                                  Parker C.T., Pradel E., Schnaltman C.A.;
"Identification and sequences of the lipopolysaccharide biosynthetic genes rfaQ, rfaP, and rfaG of Escherichia c.J. Bacteriol. 174:930-934(1992).
                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Lipopolysaccharide core biosynthesis protei
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                                                                                                                                                            SEQUENCE FROM N.A
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             Blattner F.R.;
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EMBL; M86305; AAA03743.2; -.
EMBL; U00039; AAB18608.1; -.
EMBL; AE000440; AAC76655.1; -.
EMBL; S75736; AAD43826.1; -.
ETR; B42559; B42599.
                                           Q04975;
01-NOV-1995
15-JUN-2002
15-JUN-2002
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PEMS Microbiol. Lett. 123:201-206(1994)
-i- FUNCTION: INVOLVED IN THE ADDITION
TO THE LIPOPOLYSACCHARIDE CORE.
TO THE TIPOPOLYSACCHARIDE CORE bi
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Pfam; PF00534; Glycos transf 1; 1.
Lipopolysaccharide biosynthesis; Tran-
Complete proteome.
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SEQUENCE OF 1-58 FROM N.A.
MEDLINE=95080611; PubMed=7988890;
Huisman T.T., Willemsen P.T., Appelmelk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic
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EcoGene; EG11339; rf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification by Tnio transposon reinvolved in the biosynthesis of K99 effect of LPS core mutations.";
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MEDLINE=93077458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D--KPRKFEA----LAEKLGVRSNVHFFSGRNDVSELMAAADLLLHPAY--QEAAGIVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REIYROKNGIKEQQNLLLQVGSDFGRKGVDRSIEALASLPESLRHNTL-----LFVVGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EAMAFKLPVLGTAAGGTTEIVLDGSTG--LLHPAGKEGVAPLAKNIVRLA-SHAEQRVSM
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                                        (Rel. 32,
(Rel. 41,
(Rel. 41,
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Last annotation updat
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40; Mismatches
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9 fimbriae of Escherichia coli:
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Matches 69
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CONFLICT
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MEDLINE=9332324; PubMed=8331073;
MEDLINE=9332324; No. Yokoyama H., Ezaki T.;
Hashimoto Y., Li N., Yokoyama H., Ezaki T.;
"Complete nucleotide sequence and molecular characterization region encoding Vi antigen in Salmonella typhi.";
"... Bacteriol. 175:4456-4465(1993).
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STRAIN=GIFU 10007;
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Pro; IPR001296; Glycos transf_1.
PF00534; Glycos transf_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X67785; CAA47994.1; -. D14156; BAA03195.1; -. AL627283; CAD06776.1;
                                                                                                                                                                                                                                                                                                                       Similarity
KT---QDAD---TTİGGVFRFVGDKNPFAWIDFAARYLQHH---
                                          ESLGVRSEDLLFAI INSVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVG-SDVNA
                                                                                                                      AGA--MIDSHTTAEYWNSRTSDRLKIQMPQTYVVHLGNSKELMEVAEDNVARRVLREHIR
                                                                                                                                                                                              MIALAALIAG------VPRIQLGLRGLPPV-----VRKRLFKPEYEPLYQALAVV
                                                                                                                                                                                                                                          LVILNTAVAGKWLDPVLKDHVPKV-----LPKILWWIHEMRGHYFKVEY---VKHLPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteome.
                                                                                                                                                                                                                                                                                                                                                                                      290
362
578
                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         290 S
363 KO
; 65009 MW;
                                                                                                                                                                                                                                                                                                                    4.9%;
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                                                                                                                                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                  Score 118;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                      S -> G (IN REF. 1).
KH -> ND (IN REF. 1).
; 8D420563D868C189 CRC64;
                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                       DB 1; Length 578;
                                                                                                                                                                                                                                                                                             132;
                                                                                                                                                                                                                                                                                             Indels
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1 Vi antigen
-PATRFVLVGDGDLRA
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EMBL outstation -
                                                                                         -VPHKIWQQFTQ
                                                                                                                                                                                                                                                                                             52;
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15-JUN-2002 (Rel. 35, La
15-JUN-2002 (Rel. 41, Las
EC 2.4.1.11).
(EC 2.4.1.11).
WAXY OR GBSS.
Manihot ergonical control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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Matches 56
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UGST MANES
Q43784;
Q1-NOV-1997
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94083565; PubMed=8260633; Salehuzzaman S.N., Jacobsen E., Visser R.G.F.; Salehuzzaman S.N., Jacobsen E., Visser R.G.F.; Salehuzzaman S.N., Jacobsen E., CDMA encoding granule-bound starch synthase in cassava (Manihot esculenta Crantz) and its antisense expression in potato. "; Plant Mol. Biol. 23:947-962(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manihot esculenta (Cassava) (Manioc).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnaliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Buphorbiaceae; Manihot.
                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UDP + {(1,4)-alpha-D-glucosyl}(N+1).

PATHMAY: Starch biosynthesis.

SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.

TISSUE SPECIFICITY: SYNTHESIZED IN A NUMBER OF DIFFERENT ORGEBUT MOST ABUNDANTLY IN TUBERS.

SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUT MOST ABUNDANTLY SIMILARITY: BELONGS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N)
UDP + {(1,4)-alpha-D-glucosyl}(N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         495
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                                          219
                                                                                                                                                                                                                                                                                                                                                           Pro; IPR001296; Glycos_transf_1.

Pr00534; Glycos_transf_1; 1.

gen_biosynthesis; Transferase; Glycosyltransferase;
it peptide; Chloroplast; Starch biosynthesis.

CHLOROPLAST (BY SIMILARITY).
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                                                                                                             l Similarity
56; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGVPVISTPAGGSAECFIEGVSGFILDDAQTVNLDQACRYAEKLVNLWRSRTGICQQTQS
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WNSRTSDRLKIQMPQTYVVHLGNSKELMEVAEDNVARRVLREHIRESLG--VRSEDLLFA
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                                                                                                                                                                                                                                                 96
608 AA;
                                                                                                         4.9%;
nilarity 22.6%;
Conservative 3:
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                                                                                                                                                                                                                                                                                                                                   809
                                                                                                                                                                                                                                                         66968 MW;
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Last annotation update)
n [starch] synthase, chl
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                                                                                                                 37;
                                                                                                             Score 117; DB
Pred. No. 0.16
37; Mismatches
                                                                                                                                                                                                                                                     GRANULE-BOUND GLYCO
UDP-GLUCOSE (BY SIN
; C9C970CD3011BDDB
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A NUMBER OF DIFFERENT ORGANS,
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                                                                                                                                                                                                                                                                                            ID GLYCOGEN [STARCH]
(BY SIMILARITY).
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                                                                                                                                                                               Length 608;
                                                                                                                                                                                                                                                         CRC64;
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RESULT 11
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                                                                            islets.
-!- SIMILARITY: E
-!- SIMILARITY: C
-!- SIMILARITY: C
-!- SIMILARITY: C
                                                                                                                                                                                             "Prediction of the coding sequences of unidentified human XVIII. The complete sequences of unidentified human code for large proteins in vitro.";

DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=21316449; PubMed=11294830;

Tse W.T., Tang J., Jin O., Korsgren C., John K.M., Kung A.L.,

Gwynn B., Peters L.L., Lux S.E.;

"A new spectrin, beta-IV, has a major truncated isoform that
associates with promyelocytic leukemia protein nuclear bodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9H254; Q9HCDO; Q9H3G8; Q9H1K7; Q9H1K8; Q9H1K9; I5-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spectrin beta chain, brain 3 (Spectrin, non-ery (Beta-IV spectrin) OR KIAAN1642.
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                             "BetaIV spectrin, a new spectrin localized at axon initial and nodes of ranvier in the central and peripheral nervous J. Cell Biol. 151:985-1002(2000).
                                                                                                                                                                                                                                                                                                                                                                                                        Berghs S., Aggujaro D., Dirkx R. Jr., Maksimova I
Hermel J.-M., Zhang J.-P., Philbrick W., Slepnev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                        -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1
    produced by alternative splicing.
-!- TISSUE SPECIFICITY: Abundantly expre-
                                                                                                                                                                                                                                                                   MEDLINE=20450683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M.,
                                                                                                                                                                                                                                                                                                                                                                                              Solimena M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 TO MEDLINE=20539976; PubMed=11086001
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 386-2382 FROM N.A.
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                                                                            BELONGS TO THE SPECTRIN FAMILY CONTAINS 2 CALPONIN-HOMOLOGY (( CONTAINS 1 PH DOMAIN. CONTAINS 18 SPECTRIN REPEATS.
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Query Match
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Matches 95
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PRINTS; PR00683; SPECTRINPH.
SWART; SM00033; CH; 2.
SWART; SM00033; PH; 1.
SWART; SM00150; SPEC; 16.
PROSITE; PS00019; ACTININ 1; 1.
PROSITE; PS00020; ACTININ 2; 1.
PROSITE; PS00020; ACTININ 2; 1.
PROSITE; PS00021; CH; 2.
PROSITE; PS500021; CH; 2.
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EMBL; AF00820:
EMBL; AY0042:
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EMBL; AY00426:
EMBL; AB04668
HSSP; Q01082;
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   95;
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                 Similarity
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IPR001605;
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                                                AVTRILLEK -> MPHYPSC

AMPKILDQLEIQH -> CLIIHPALLAHPPWE

MISSING (IN ISOFORM 2).

IEKIKAEQSKOPPTPLEARFGDPTELAAKAAPLLRPGGY
E -> PERRBHLINGOVDOPWOHTEKPSLPKPKANKEKTAR

RDGTCL (IN ISOFORM 4).

MISSING (IN REF. 2).

MISSING (IN REF. 2).

714 L -> S (IN REF. 2).

89 E -> K (IN REF. 2).

80 G -> S (IN "EF")

9982 PM; E^^
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SPECTRIN 3.

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SPECTRIN 10.

SPECTRIN 11.

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SPECTRIN 13.

SPECTRIN 16.

SPECTRIN 16.

SPECTRIN 17.

SPECTRIN 17.

SPECTRIN 18.

PH.

MISSING (IN ISOFORM 3).

AVQAAEGLLAQGNIYGEQAGAGATRLLEK -> MPHYDSCS
SAPSLOTEIPOPIOQLEANHR (IN ISOFORM 3).

NOENQLRAGOMMQKLHDQLELQH -> CLIIHPALLHPPWE
PPYLPRSSS (IN ISOFORM 2).
   58;
Score 112.5; |
Pred. No. 2.7;
58; Mismatches
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CH 1.
CH 2.
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                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; X03935; CAA27574.1; -. EMBL; M24258; AAA33520.1; -. PIR; S07314; S07314.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Schwarz-Sommer Z., Saedler H.;
Kloesgen R.B., Gierl A., Schwarz-Sommer Z., Saedler H.;
Kloesgen R.B., Gierl A., Schwarz-Sommer Z., Saedler H.;
Mol Gen. analysis of the waxy locus of Zea mays.";
Mol Gen. Genet. 203:237-244(1986).
I-I-FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
I-I-CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N-1).
IDP + {(1,4)-alpha-D-glucosyl}(N+1).
IDP + {(1,4)-alpha-D-glucosyl}(N+1).
I-I-PANTHWAY: Starch biosynthesis.
I-I-SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
I-I-SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGST_MAIZE STANDARD; PRT; 605 AA. P04713; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Granule-bound glycogen [starch] synthase, chi(EC 2.4.1.11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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CHLOROPLAST.
Transit peptide; Chloroplast; Starch biosynthesis.
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STRAIN=1021;
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MEDLINE=21101807; PubMed=11157937;
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Bacteria; Proteobacteria; alpha subdivision;
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                                                                                                                     PATHWAY: Lipopolysaccharide core biosynthesis.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Extended the Composan Bioinformatics Institute. There are no resurby non-profit institutions as long as its content
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                                                                    STRAINE-CV. Vogelsanger Gold; TISSUE-Lea MEDLINE-88303345; PubMed=2970062; Rhode W., Becker D., Salamini F.; "Structural analysis of the waxy locus Nucleic Acids Res. 16:7185-7186(1988).
                                                                                                                                                             Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Stra
Spermatophyta; Magnoliophyta;
Triticeae; Hordeum.
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                      STRAIN=cv. H354-295-2-5;
MEDLINE=94170739; PubMed
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=4513;
                                               SEQUENCE OF 76-89
                                                                                                                                                                                                                                                                                          HORVU
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76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMLNHGVQVLPARGQEAVDIA-----
                                                                                                                                                                                                                                                                                                                                                  RGHETLVGQFSREAITDAYLQLL
                                                                                                                                                                                                                                                                                                                                                                                              EAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAG-KEGVAPLAKNIVRLASHAEQRVSMGE
                                                                                                                                                                                                                                                                                                                                                                                                                                            ERDNLHKLATDL-----GVSGRVRFAGWQDDTRPFLAAVDVFVMSSS--HEPLGNVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAQT--KFETQLRDFVVKNTIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFAIINSVSRGK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSYF--RNTDCIVCNTPGIAERVSDLGWKREIRVISNFTGTGRVV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEYWNSRTSDRLKIQMP--QTYVVHLGNSKELMEVAEDNVARRVLREHIRESLGVRSEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDPVLKDHV-----PKVLPKILWW---IHEMRGHY---FKVEYVKHLPFVAGAMIDSHTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFFVHLVNALAERGVEQTAIIRPGRGWRRDIEGAAKIRESHFRNLSLDRILL-
                                                                                                                                                                                                                                                                                                                                                                       KGYGRVKEMFMEHHMAERIAAVL 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --PLKVKHMARREKPDVL---MAWAPRASELMPNYKGAFKISRLGDYP
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  of acidic barley endosperm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVDRAKLDTPADAPVVMSMGRFVERKGFHTLIEAV----ARLPGVYLWLLGDGE
                       95-2-5; TISSUE=Starchy PubMed=8125056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38036 MW;
                                                                                                                                                                                                                                [starch]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                        Streptophyta; Embryophyta;
yta; Liliopsida; Poales; Po:
                                                                                                                                                                                                                                          sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 107; DB Pred. No. 0.44;
                                                                                                                  TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D8363F95FD9E169F CRC64;
                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                synthase,
                                                                                                                                                                                                                                                                                                                                                  336
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 proteins by
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                                    endosperm
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                                                                               Hordeum vulgare.
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                                                                                                                                                                           Poaceae;
  two-dimensional
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                                                                                                                                                                                                                                precursor
                                                                                                                                                                           Pooideae;
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ib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Query Match
Best Local
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027830;
15-DEC-1998 (
15-DEC-1998 (
15-JUN-2002
                                                                                                                                                                                                                                                                                                    HELX_METTH
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Pfam; PF00534; Glycos transf 1; 1.

Glycogen biosynthesis; Transferase; Glycosyltransferase;
Transit peptide; Chloroplast; Starch biosynthesis.

TRANSIT 72

CHLOROPLAST (BY SIMILARITY)

CHAIN 73 603

CRANULE-BOUND GLYCOGEN (BY CHAIND TYP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
STRAIN=Delta
                                                                                                                                                                       Archaea; Euryarchaeota;
Methanobacteriaceae; Me
                                                                                                                                                          NCBI_TaxID=187420
                                                                                                                                                                                                    Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                               Putative ATP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X07931; CAA30755.1; -.
EMBL; X07932; CAA30756.1; -.
PIR; S01727; YUBHY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIILLGT---GKKKFEKLLKSMEEK-----FPGKVRAVVRFNAPLAHQMMAGADLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAVVVGSDVNAQTKFETQLRDFVVKNTIHDRVHFVNKTLAVAPY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603 AA;
                                                                                                                                                                                                                                             (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 41, Last annotation updat
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90
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66211 MW;
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                                                                                                                                                                        ta; Methanobacteria; Methanobacteriales;
Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                  [QLQGMRYGTPCVCASTGGLVDTIVEGKTGFHMGRLSVDCNVVEPADV
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRANULE-BOUND GLYCOGEN [STARCH]
UDP-GLUCOSE (BY SIMILARITY).
; 0B0B3DE6A8217934 CRC64;
                                                                                                                                                                                                                               MTH1802
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                                                                                                                                                                                                                                                                                                      862
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                           Prabhakar S.,
                                                    Ď.,
                                                                                     Dubois
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Search completed: June Job time : 24 secs

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Hydrolase; Helicase; ATP-binding; Complete proteome.

NP BIND 54 61 ATP (POTENTIAL).

SITE 178 181 DEIH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                            445
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532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00270; DEAD; 1.
PF00271; helicase C; 1.
; SM00487; DEXDC; 1.
; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 ALRDPCDGRGDPAALNTAVASGSPLGFMRSKLVLLVSHELSLSGGPLLLMELAFLLRHVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99;
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EDFME
                            EMFME
                                                           EYVELEERYVYAKIWVDYDKNQFGKRGKLARMLYSTNIGTIPDRSAAVVKCGGKVVGRIE
                                                                                      GTTE----IVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVK
                                                                                                                     PENCLDVLAQHIYGMAIENPWDIDHALAVIRNSY---
                                                                                                                                                  ----KTLAVAPYLAAID-----VLVQNSQGRGECFGRITIEAMAFKLPVLGTAAG
                                                                                                                                                                                 KSVSRALQRIGRSGHQLHQRSKGRIVVVDRDDLVEC-----SLILKNALEGKIDSIKV
                                                                                                                                                                                                            QAFYQALQLI----QHEKLKVPRIHAVVVGSDVNAQTKFETQLRDFVVKNTIHDRVHFVN-
                                                                                                                                                                                                                                               SREIRLETEEKLKRGELK-----
                                                                                                                                                                                                                                                                           SKELMEVAEDNVARRVLREHIRESLGVRSEDLLFAIINSVSRGKGQDLFL------
                                                                                                                                                                                                                                                                                                                        YGSERECLIVDVSYLKELDIDLICPVDDIVAA---DP---EEIGNALYDIL---HDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                STVRYVIVDEIHSLADNKRGVHLSLSLERLQHLVGDFTRIGLSATVHPLERVARFLVGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQVVWI----TNQRSQETNDVTYSLEHRMLNHGVQVLPARGQEA-------
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IPR001650;
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536
                            449
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DEIH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 107;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                             AVVSSTSLELGIDIGYIDLVVLLSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                     CYRNLSREDY --- LSVLSYLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 140;
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 0.5
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SPTREMBL 21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
10: sp_blant:*
11: sp_rodent:*
11: sp_virus:*
2: sp_virus:*
4: sp_unclassified:*
4: sp_morlassified:*
5: sp_bacteriap:*
5: sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        June 30, 2003, 16:18:51; Search time 36 Seconds (without alignments) 2707.230 Million cell updates/sec
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2397
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | · UT | 4 | w | N | ۲ | Result | • |
|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------------|---|
| 165 | 166 | 169.5 | 172.5 | 179.5 | 180 | 181.5 | 182.5 | 187.5 | 197 | 207 | 482.5 | 487 | 671 | 1471 | 1478 | Score | |
| 6.9 | 6.9 | 7.1 | 7.2 | 7.5 | 7.5 | 7.6 | 7.6 | 7.8 | 8.2 | 8.6 | 20.1 | 20.3 | 28.0 | 61.4 | 61.7 | Query Match I | ж |
| 471 | 382 | 381 | 370 | 424 | 412 | 381 | 424 | 388 | 416 | 382 | 670 | 697 | 188 | 458 | 402 | Query Match Length DB | |
| ω | 16 | N | 16 | v | 17 | 17 | ű | 16 | 17 | 16 | 10 | 10 | 10 | 10 | 10 | 8 | |
| Q8X0H8 | C87 QW3 | Q9EVX4 | Q9PEZ9 | 80ZV6Ö | Q9HH00 | 059512 | Q95SA2 | 06ZM6Ö | 058762 | Q8UA15 | Q9SSP6 | Q9LSB5 | Q9LI48 | Q9FXG9 | Q9FWT0 | ĬĎ . | |
| Q8x0h8 neurospora | Q8yqw3 anabaena sp | Q9evx4 streptococc | Q9pez9 xylella fas | Q9vzu8 drosophila | Q9hh00 pyrococcus | 059512 pyrococcus | Q95sa2 drosophila | Q9wz90 thermotoga | 058762 pyrococcus | | | Q9lsb5 arabidopsis | Q9li48 oryza sativ | Q9fxg9 arabidopsis | Q9fwt0 arabidopsis | Description | |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 |
|--------------------|--------|--------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------|--------|-------------------|--------|--------------------|--------|--------------------|--------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|--------|--------|--------------------|
| 144 | 144 | 144 | 145 | 147 | 147.5 | 147.5 | 148.5 | 148.5 | 148.5 | 149 | 149.5 | 150 | 151 | 151.5 | 151.5 | 154 | 154 | 154.5 | 155 | 156 | 157 | 157.5 | 161 | 161 | 162.5 | 163 | 163 | 163.5 |
| 6.0 | 6.0 | 6.0 | 6.0 | 6.1 | 6.2 | | | | 6.2 | | 6.2 | | 6.3 | 6.3 | 6.3 | 6.4 | 6.4 | 6.4 | 6.5 | 6.5 | 6.5 | 6.6 | 6.7 | | | | 6.8 | 6.8 |
| 429 | 425 | 409 | 3.95 | 333 | 380 | 351 | 436 | 383 | 378 | 381 | 393 | 406 | 375 | 414 | 411 | 422 | 358 | 351 | 290 | 416 | 511 | 506 | 405 | 380 | 385 | 422 | 404 | 360 |
| 16 | N | 16 | 16 | 17 | N | 16 | 16 | 2 | 16 | 16 | 16 | 16 | 16 | 16 | 17 | N | 17 | 17 | N | 16 | w | w | 10 | 16 | N | 16 | 16 | 17 |
| Q8YRS3 | Q939V0 | Q55598 | Q9K6L7 | Q9HSV4 | 068201 | Q8UDE4 | Q9KYG6 | Q9RHD1 | Q9HUG1 | Q8Z2F9 | Q9WZ95 | Q8RBZ4 | Q9KC90 | Q92QS8 | 026550 | Q937E1 | 8nz18Ö | Q58577 | Q8VW73 | Q92VR7 | Q96WW6 | 013604 | 86AZ6Ö | Q8RBZ6 | Q9X4V1 | Q98J63 | Q8RCY0 | Q8ZZ46 |
| Q8yrs3 anabaena sp | a | | Q9k617 bacillus ha | | O68201 escherichia | | Q9kyg6 streptomyce | Q9rhdl pseudomonas | | | Q9wz95 thermotoga | | Q9kc90 bacillus ha | | O26550 methanobact | - | Q8tzu8 pyrococcus | Q58577 methanococc | Q8vw73 pasteurella | Q92vr7 rhizobium m | Q96ww6 schizosacch | ß | | σ | Q9x4v1 streptococc | | | Q8zz46 pyrobaculum |

ALIGNMENTS

| 137 | 78 TSLKADLIVLNTAVAGKWLDAVLKENVVKVLPKILWWIHEMRGHYFNADLVKHLPFVAGA | Дb |
|-----|--|----------|
| 208 | 149 IALKADLVILNTAVAGKWLDPVLKDHVPKVLPKILMWIHEMRGHYN VEYVKHLPFVAGA | Ş |
| 77 | 18 SRGPLLLMELAFILRGVGADVVWITNQKFLEDDEVVYSLEHKMLDRGVQVISAKGQKAVD | В |
| 148 | LNHGVQVLPARGQEAVD | δ |
| 0; | es 283; Conservative 53; Mismatc | 3 |
| | Query Match 61.7%; Score 1478; DB 10; Length 402; Best Local Similarity 74.5%; Pred. No. 1 6e-107; | w ro |
| | SEQUENCE 402 AA; 44901 MW; 5B2D117CD4E13DD5 CRC64; | SQ |
| | Pfam; PF00534; Glycos_transf_1; 1. | 닮 |
| | EMBL; AC023754; AAG13070.1; | ı R |
| | L/GenBank/DDBJ databases. | RL |
| | umi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R. | RA |
| | Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., | ₽3 |
| | Tobraco V., CHIH C., CHIOU J., CHOI | 2 3 |
| | Altaii H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., | P R |
| | Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., | RA |
| | SEQUENCE FROM N.A. | RP |
| | [1] | RN |
| | NCBI TaxID=3702; | õ |
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| | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | 8 |
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| | Arabidopsis thaliana (Mouse-ear cress). | SO |
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| | (TrEMBLrel. 16. | ΡŢ |
| | 01-MAR-2001 (TrEMBLrel. 16, Created) | ΡŢ |
| | | AC |
| | O9FWTO PRELIMINARY: PRT: 402 AA. | IJ, |
| | RESULT 1 | OFF |
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Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Honz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P. Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W., Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AC007797; AAG12556.1; -

InterPro, IRR001296; Glycos transf_1, 1.

Ffam; PF00534; Glycos transf_1; 1.

SEQUENCE 458 AA; 51367 MW; 609AlB9DBB818740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledoms; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                    LKDHVPKVLPKILWWIHEMRGHYFKVEYVKHLPFVAGAMIDSHTTAEYWNSRTSDRLKIQ
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LKDNVPKVLPKVLWWIHEMRGHYFKPDLVKHLPFVAGAMIDSHATAEYWKVRTHDRLGIK
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                                                                                                                        WITNORSQETNDVTYSLEHRMLNHGVQVLPARGQEAVDIALKADLVILNTAVAGKWLDPV 170
                                                                                                                                                             REKEDNSDIKIOSVSGSLNPLEFMKSKLVLLVSHELSLSGGPLLLMELAFILRGVESEVV 110
                                                                                                                                                                             ----DPAALNTAVASGS--PLGFMRSKLVLLVSHELSLSGGFLLLMELAFLLRHVGSQVV 110
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                  MPQTYVVHLGNSKELMEVAEDNVARRVLREHIRESLGVRSEDLLFAIINSVSRGKGQDLF
                                                                                                         WITNOKPVEEDEVIKVLEHKWLDRGVOVISAKSOKAIDTALKSDLVVLNTAVAGKWLDAV 170
                                                                                                                                                                                                                 MAKPSTSMWATLQKKRWP-----LMILLV---LSVSTVGMILVRSTFDSCSVSGKRCS
                                                                                                                                                                                                                                          MAKTPSFAVAAVAGGRGPVHNRTQLLLLLLVAVAASASTAGFLLRGALRDPCDGRG----
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    MPKTYVVHLGNSKELMEVAEDSFAKNVLR--
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65; Mismatches
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Q91148;
Q91148;
Q1-QT-2000 (TrEMBLrel. 15, Created)
Q1-QT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QT-2001 (TrEMBLrel. 17, Last annotation update)
Q1-QT-2001 (TrEMBLrel. 17, Last annotation update)
EST C74729 (E30675) corresponds to a region of the predicted gene.
Oryza sativa (Rice).
Cryza sativa (Rice).
Cryza sativa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
UCBI TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP001366; BAA9249.1; -.
InterPro; IPR001296; Glycos transf_1.
Pfam; PF00534; Glycos transf_1; 1.
SEQUENCE 188 AA; 20622 MW; C7C4E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
clone:P0469E09.";
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                                                                                       DRVSMGRKGYGRVKEMFMEHHMA
                                                                                                                     QRVSMGEKGYGRVKEMFMEHHMA
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Q9LSB5 PRELIMINARY; PRT; 697 AA.

Q9LSB5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
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Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
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Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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InterPro; IPR001296; Glycos_transf_1.
Pfam; PF00534; Glycos_transf_1; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
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GRVKEMFMEHHMAERIAAVLKDVLR |::|:|:|:||:||:||:||
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                                                                      -KVAYVKEMLSFLSNNGNLSNSVLWTPATTRVASLYSAADVYVTNSQGVGETFGRVTIEA
                                                                                                                                                                                            AQTKFETQLRDFVVKN-TIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEA
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
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RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
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RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
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Best Local
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"Arabidopsis thaliana chromosome 1 BAC F6D8 sequence.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
F6DB.36 protein (Glycosyl transferase, putative).
F6DB.36 OR F19K6.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=CV. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO01199; Cyt_B5.
InterPro; IPRO01296; Glycos transf_1.
Ffam; PF00534; Glycos transf_1; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G
                                                                                                                      193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC008016; AAD55621.1; -. AC037424; AAG51540.1; -.
                                                           81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408:816-820(2000).
LLFHELSMTGAPISMMELASELLSCGATVSAVVLSRRG-----GLMQELSRRRIKVVE
                                                           LVSHELSLSGGPLLLMELAFLLRHVGSQVVWITNQRSQETNDVTYSLEHRMLNHGVQVLP 140
                                                                                                                             ATYGKLLGPFGSLEDKVLEWSPHRRSGTCDRKSD.
                                                                                                                                                                                     STAGELLR--GALRD-----PCDGRGDPAALNTAVASGSPLGFMR---SKLVL
                                                                                                                                                                                                                                                                                                                                                                                        670
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                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                   20.1%;
                                                                                                                                                                                                                                                       77;
                                                                                                                                                                                                                                                    Score 482.5;
Pred. No. 3.6e
77; Mismatches
                                                                                                                                                                                                                                                                                       3.6e-29;
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Sakano
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Aakenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchoud C., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21608550; PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                   "Genome sequence of the plant pathogen and Agrobacterium tumefaciens C58."; Science 294:2323-2328 (2001).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=21608551; PubMed=11743194;
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Chumley F., Tingey
Nester E.W.;
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Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-JUN-2002 (TrEMBLrel. 21, Ol-JUN-2002 (TrEMBLrel. 21, Ol-JUN-2002 (TrEMBLrel. 21, Glycosyltrenseforar)
                                   EMBL; AE009285; AAL44372.1; -.
EMBL; AE008327; AAK89838.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome of the natural genetic engineer
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     Complete
        proteome
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alpha subdivision; Rhizobiaceae
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Last annotation updat
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                                                                                                                                            biotechnology agent
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Gordon L.
Gerry M.,
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
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Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Yamamoto S., Sekine M., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y. Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya N., Oguchi Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             058762;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus horikoshii.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              058762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thermophilic archaebacterium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Complete sequence and gene organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Res.
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                                                                                                                                                                                                                                                                                                          104;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Pro; IPR001296; Glycos transf_1.
PF00534; Glycos_transf_1; 1.
PF00534; Glycos_transf_1; 1.
hetical protein; Complete proteome.
NCE 416 AA; 48196 MW; 89BDBEE51E1CE7B0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP000004; BAA30133.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                        Similarity
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VAGAMID-SHTTAEYWN-----SRTSDRLKIQMPQTYVVHLGNSKELM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5:55-76 (1998)
                                                                                   SLKLTEEMKELYLNVNRENSKFIDLSSFDYV-----LVHDPQPAALIEFYEKKSPW
                                                                                                                                         AVDIALKADLVILN-TAVAGKWLDPVLKDHVPKVLPKILWWIHEMRGHYFKVEYVKHLPF
                                                                                                                                                                                                 SFGGGVAEILHSLVPLLRSIGIEARWFVIEGPTEFFNVTKTFHNAL
                                                                                                                                                                                                                                                    SLSGGPL-LLMELAFLLRHVGSQVVWITNQRSQETNDVTYSLEHRMLNHGVQVLPARGQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLGLDGRVRFLGFRSDVPELMASMDVVAHTSI-VAEPFGRVVVEAMMCGRPVVATRGGGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (TrEMBLrel. 07,
3 (TrEMBLrel. 07,
2 (TrEMBLrel. 20, 3)
al protein PH1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382
                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑA.
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                                                                                                                                                                                                                                                                                                                                     8.2%;
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27.5%;
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                                                                                                                                                                                                                                                                                                             56;
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Last annotation update)
                                                                                                                                                                                                                                                                                                          Score 197; DB 17;
Pred. No. 4.1e-07;
56; Mismatches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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Pred. No. 5.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus
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                                                                                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the genome of a hyper-
horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
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MEDLINE-99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Haft D.H., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
McDonald L., Utterback T.R., Malek J.A., Phillips C.A., Richardson D.,
Slewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001296; Glycos transf 1.
Pfam; PF00534; Glycos transf 1; 1.
Complete proteome.
SEQUENCE 388 AA; 43648 MW; 6BAA1BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001736; AAD35706.1; -. TIGR; TM0622; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipopolysaccharide biosynthesis protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAAIDVLVQNSQGRGECFGRITIEAMAFKLFVLGTAAGGTTEIVLDGSTGLLHPAGKEGV
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVPRIHAVVVG----SDVNAQTKFETQLR----DFVVK---NTIHDRVHFVNKTLAVAPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARR----VLREHIRESLGVRSEDLLFAIINSVSR----GKGQDLFLQAFYQALQLIQHEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWRCHIDLSSPNREFWEFLRRFVEKYDRYIFHLPEYVQPELDRNKAVIMPPSIDPLSEKN
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                                                                                                                                                                                                                                                                                                                  VQVLPARGQEAVDIALKADLVILNTAVAGKWLDPVLKDHVPKVLPKILWWIHEMRGHYFK 195
TIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTTE
                                                                                       INSVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVGSDVNAQTKFETQLRDFVVKN
                                                                                                                            AFKFFGFVPVSISQEVAESVKKLYGRKISTPVIYNGIDVQKFSIDQPKRVDRDKTILINV
                                                                                                                                                                                                                                            VEYVK-----HLPFVAGAMIDS-----
                                                                                                                                                                     QMPQTYVVHLGNSKELMEVAEDNVARRVLREHIRESLGV-----RSEDLLFAI
                                                                                                                                                                                                          LREIRPDIIHSHLSALRIALIPALLCRIPVKVHTIHTVAEKDAKGITRFFN-----
                                                                                                                                                                                                                                                                                   VEKLTSKGYQVYTIVLDYE-----AIAPS-----KVIRRLLRAIKNMRRTYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
(Tremblrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  388 AA; 43648 MW; 6BAA1BE01157F306
                                                                                                                                                                                                                                                                                                                                                         7.8%; ilarity 23.5%; Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - FGLTVTEAMWKGKPVIGRAVGGIKFQIVDGETGFLVRDANBAV
                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                             Score 187.5; DB Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                           ---SCPNLELWLVGDG-----ELRRDIEELVKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                             136;
                                                                                                                                                                                                                                                -HTTAE-----YWNSRTSDRLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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                                                                                                                                                                                                                                                                                                                                                                 93;
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Q95SA2
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01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C., Nunco J., Paceleb J., Paragas V., Park S., Phouanenavong S., Wayn C., Lewis S.E., Rubin G.M., Celniker S.; Yu C., Lewis G. Rubin G.M., Celniker S.; Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Inse
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Ephydroidea, Drosophilidae, Drosophila.
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SEQUENCE
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FIyBase; FB9n0035401; CG1291.
InterPro; IPR001296; Glycos transf_1.
Pfam; PF00534; Glycos transf_1; 1.
SEQUENCE 424 AA; 48639 MW; F39F08BF7A11BE35 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLFLHPDLGIGGAERLVVDAALALKERGHQVSFLTNHHDSTHCFKETADGTFPV-----
                                                                                                                                                                             QTKFETQLRDFVV-----KNTIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRIT 377
                                                                                                                                                                                                                  LDINRYERKKNHALALHSLRLLGDMLPATEFK--RCRLIIAGGYDTRCMENVEHFAELEH 283
                                                                                                                                                                                                                                                       AIINSVSRGKGQDLFLQAFYQALQLIQHEKLKVPRIHAVVVG----
                                                                                                                                                                                                                                                                                         SKFTLRVFQDTFRRLSTVPDVLYPSLHTQYFDQMQKKLEQRSALLDEPVHPRVPLNAFIY 225
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                                                                                                                                                                                                                                                                                                                                                                   LRFAPHRPKVLFYCHFP------DOLLSSREGLLKRLYRLPINWLEEHTIGLADKVLVN 165
              KGYGRVKEMFMEHHMAERIAAVLKDVLRKSQEHS
                                                                                               IBAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAPLA
                                                                                                                                            LTE-ELKLODHVVLLRSPTDEEKCRLLFAAHCLLYTP-
                                                               LEGMYCSKPVVALNSGGPTETVVNTSTGFLCEKTEKS---F AMLQLFRDEQLRVKMGD
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Pred. No. 5.8e-06;
5; Mismatches 179;
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Query Match

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RESULT 11
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01-MAR-2001
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InterPro; IPR001296; Glycos transf_1.
Pfam; PF00534; Glycos transf_1; 1.-.
Hypothetical protein; Complete proteome.
SEQUENCE 381 AA; 42826 MW; EDOEBOCAOCFSCAE1 CRC64;
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01-AUG-1998 (TrEMBLrel. 07,
01-MAR-2002 (TrEMBLrel. 20,
Hypothetical protein PH1844.
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Archaea; Euryarchaeota;
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                                                                                                                                                                                                                          LASHAEQRVSMGEKGYGRVKEMFMEHHMAERIAAVLKDVLRK 466
                                                                                                                                                                                                                                                                              IS---SEAFGIVILEAMASGVPIIATDVGGIPEVIKENSAGLLVPPGNE--LKLREAIEK
                                                                                                                                                                                                                                                                                                                              NSQGRGECFGRITIEAMAFKLPVLGTAAGGTTEIVLDGSTGLLHPAGKEGVAPLAKNIVR 424
                                                                                                                                                                                                                                                                                                                                                                                    DATLYMVGNGEMLPFLKAQTKF-----LGIENKVVFMGYVPDDILPEVFRMADVFVLPS
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23.1%; Pred. No. 5.9e-06
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RESULT 12 Q9VZU8 ID Q9VZU AC Q9VZU

Q9VZU8

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Best Local S
Matches 99
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EMBL; AP3010272; AAL81866.1; -.

EMBL; AP307053; AAG45391.1; -.

EMBL; AP307052; AAG45391.1; -.

EMBL; AP307052; AAG45375.1; -.

InterPro; IPR001296; Glycos transf_1; 1.

Pfam; PF00534; Glycos transf_1; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 412 AA; 48017 MW; 6A5338298A6B5CEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=P.furiosus, and T.litoralis;
MEDLINE=20566786; PubMed=11115105;
Diruggiero J., Dunn D., Maeder D.L., Holley-Shanks R., Chatard J.,
Horlacher R., Robb F.T., Boos W., Weiss R.B.;
"Evidence of recent lateral gene transfer among hyperthermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-P.furiosus; STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCI Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The Complete sequence of the Pyrococcus furiosus genome."; Summitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TIEMBLrel. 16, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
Putative trehalose synthase.
pF1742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus furiosus, and Thermococcus litoralis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                             457
 406
                                                             350
                                                                                         397
                                                                                                                       300
                                                                                                                                                     337
                                                                                                                                                                                   244
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                                                                                                                                                                                                                                                                                                  142 ---YEKRQPWIWRCHIDLSDPNLEFWKFL---RQFVEKYDRYIFHMEEYVQEDLNQEKVV
                                                                                                                                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                                                                                                                                                                   139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 SLSGGPL-LLMELAFLLRHVGSQVVWITNQRSQETNDVTYSLEHRMLNHGVQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99;
TTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                             AAVL 460
                                                                                 EIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAERI
                                                                                                                                             NTIHDRVHFVNKTLAVAPYLAAIDVLVQNSQGRGECFGRITIEAMAFKLPVLGTAAGGTT 396
                                                                                                                                                                                                                                       IMPPSIDPLSEKNMELSESEILKTLERFDV-----DPERPIITQVARFDPWKG---
                                                      LQIVDGKTGFL----VKDVNDAIEKTLYLLEHKDVAQEMGKNAKERIKENFIITKHLERY
                                                                                                                       TGVHAR----
                                                                                                                                                                            ----VFDVIDVYRKVKEKIPEVQLLLVGVMAHDDPEGWIYFEKTLRKIGEDYDIKVLTNL
                                                                                                                                                                                                         FLQAFYQALQLIQHEKLKVPRIHAVVVG----SDVNAQTKFETQLR----DFVVK----
                                                                                                                                                                                                                                                                   -----SKELMEVAEDNVARRVLREHIRESLGVRSEDLLFAIINSVSR---GKGQDL
                                                                                                                                                                                                                                                                                                                                KVEYVKHLPFVAGAMID-SHTTAEYWNSRTSDRLKIQMPQTYVVHLGN------
                                                                                                                                                                                                                                                                                                                                                              KLYLEINKKNAEDIDLTQFDYVLI-------
                                                                                                                                                                                                                                                                                                                                                                                                                       ŚFGĠĠVAEILHNĹVPĹMRDVĠIDARŴFVIEGTNEFFNVTKŚF-HNALQGNKELRLTEEMK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 180;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17;
.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158;
                                                                                                                  - FGLTVTEAMWKEKPVVGRAVGGIK
                                                                                                                                                                                                                                                                                                                                                                -HDPQPAPLIEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 112;
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RX MEDLINGE 2019506; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Golle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Abril J.F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Bauk A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Berloon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Bellew R.M., Bauk A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Berloon R.V., Bernan B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., RA Belson K.Y., Benos P.V., Bernan B.P., Bhandari D., Botshakov S., RA Gerband B., Belchar A., Deng Z., Mays A.D., Dev I., Dietz S.M., Davits P., Botcher A., Chandra I., Cadieu E., Center A., Chandra I., Charly J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Grabios B., Delchar A., Deng Z., Mays A.D., Dev I., Dietz S.M., Dosoler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Dodson K.A., Bouph L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dolson K., Googe F., Gorrell J.H., Gu Z., Guan P., Harris M., Jalaii M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalaii M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Mansarman D.A., Weinstock M.P., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muray D.M., Noshrefi A., Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Mang
Query Match
Best Local Sim
Matches 101;
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01-MAY-2000
01-MAR-2002
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NGBI TaxID=7227;
                                                                                                                                                                                                                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fri George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Li Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubi
                                                                                                EMBL; AE003477; AAF47719.1; -.

EMBL; AV071629; AAL49251.1; -.

FlyBase; FBgn0035401; CG1291.

InterPro; IPR001296; Glycos transf 1.

Pfam; PF00534; Glycos transf 1; 1.

SEQUENCE 424 AA; 48598 MW; 9F77DA4A610DAB34 CRC64;
                                                                                                                                                                                                            EMBL; AE003477;
EMBL; AY071629;
                                                                                                                                                                                                                                                         Celniker S.;
Submitted (DEC-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein (RE67594p).
                            Similarity
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(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 20, Last annotation)
Conservative
                      7.5%;
  73;
Score 179.5;
Pred. No. 9.9e
73; Mismatches
                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                         .9e-06;
                                                DB 5;
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                                                Length 424;
  Indels
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Prise E.
Liao G.,
Park S.,
in G.M.,
99;
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TOTO CON SONO PROPERTIES DE CONTROL DE CONTR

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RX MEDLINE-20365717; PubMed=10910347;
RX MEDLINE-20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bave J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa N.C.R.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fagariser M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambals M.R., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambals M.R., Leite L.C.C.,
RA Krieger J.E., Lemos M.V.F., Lopes C.A., Machado J.A.,
Marchado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.I., Martins E.M.F., Marsucado J.A.,
Marques M.V., Martins E.A.I., Martins E.M.F., Marsucado J.A.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.G., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Miracca E.G., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Oliveira R.C., Palmeri D.A., Paris A.,
RA Menck C.F., do Silveira R.C., Palmeri D.A.,
RA Menck C.F., do Silva R.G., Santelli R.V., Sawasaki H.E.,
RA Heixed V.E. J., de Soa R.G., Santelli R.V., Sawasaki H.E.,
RA Gensoa V.E. J.T., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA Gensoa V.E. J.T., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Rosa V.E. J.T., de Sa R.G., Santelli R.V., Sawasaki H.E.,
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Q9PEZ9;
01-OCT-2000
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIINSVSRGKGODLFLQAFYQALQLIQHEKLKVPRIHAVVVG----
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation updatcharide biosynthesis protein.
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MEDILINS=20519245; PubMed=11065358;

MEDILINS=20519245; PubMed=11065358;

Almiron-Roig E., Mulholland F., Gasson M.J., Griffin A.M.;

Almiron-Roig E., Mulholland F., Gasson M.J., Griffin A.M.;

"The complete cps gene cluster from Streptcoccus thermophilus NCFB
2393 involved in the biosynthesis of a new exopolysaccharide.";
2393 involved in the biosynthesis of a new exopolysaccharide.";

Microbiology 146:2793-2802(2000).

EMBL; X17900; CAC18357.1; -

EMBL; Y17900; CAC18357.1; -

Theory IPR001296; Glycos transf_1.

Pfam; PF00534; Glycos_transf_1; 1.
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RABLE, AE003927, ARB93689.1; -...
InterPro; IPR001296; Glycos transf_1.

Pfam, PF00534; Glycos transf_1.

Complete proteome.
                                                                                                                   Transferase.
SEQUENCE 381 AA; 42630 MW; 995210276BD179AC CRC64;
                                                                                                                                                                                                                                                                                                                                                              Streptococcus salivarius.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                Streptococcaceae; Streptococcus.
NCBI_TaxID=1304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Putative hexose transferase
                                                                Local Similarity 25.5%; tes 76; Conservative
 104
                                  160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 7.2%; Score 172.5; DB 16; Length Similarity 25.0%; Pred. No. 2.9e-05; 79; Conservative 48; Mismatches 136; Indels
TAVLEGIYLKRKLK-----LP-LIWHVHEI---IVKPKAISDFINELMGRYADTIVTV- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAVSAYARRHYLAEGMPPERVQVLYNPVDTDALRPDPRVRRAMLHE-----LGWDEDVLV 185
                              TAV-AGKWLDPVLKDHVPKVLPKILWWIHEMRGHYFKVEYVK-HLPFVAGAMIDSHTTAE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIAAVLKDVLRKSQEH 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAETLQDGTTGMLLPAGD---VPAWRNAILAFCDPQPRAAMAAAAPSFVEARFSQQVIAA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGCFGRIHEGKGVFVLAEAMEQAMQ-----EEPRICCLWMGTGLHVQ-----RLAATV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHPDVLVGDFGKEYWPLLLMGRLYRLPVVLFRHRLP-----PMNCFSTYWVPRLADRF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFISELERVI -- SDRH 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTEIVLDGSTGLLHPAGKEGVAPLAKNIVRLASHAEQRVSMGEKGYGRVKEMFMEHHMAE 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGSRFASRORVLGWVTDPÁRYFQÁLAMLAMPSL-LPÉTFGRVSAEÁQÁSGVPVLVSDVGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------LKIQMPQTYVVHLGNSKELMEVAED-NVARRVLREHIRESLGVRSEDLL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 AA; 41001 MW; 57E3151F08B85510 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                              7.1%; Score 169.5; DB 2; Length 381; 25.5%; Pred. No. 5.1e-05; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
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                                                                Indels 45;
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                                                                Gaps
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| Search completed: . Job time : 41 secs | 368 N | 436 GI | 308 K |
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| Search completed: June 30, 2003, 16:27:36 Job time : 41 secs | | | 308 KAGGAMELVEHGVNGFLTTPGESQELANIINTCIEDTQKTATIASNAQAIASQRFDVVTI 367 |
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